

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:33:43 ; Search time 119 Seconds
(without alignments)
34.425 Million cell updates/sec

Title: US-10-036-918B-4
Perfect score: 33
Sequence: 1 XPXRPYXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	90.9	269	2 Q7NFB5	Q7NFB5 glieobacter
2	30	90.9	286	2 Q96WP3	Q96WP3 arthroderma
3	30	90.9	295	2 P95666	P95666 rhizobium 1
4	30	90.9	320	2 Q98KT4	Q98KT4 rhizobium 1
5	30	90.9	325	2 Q8EH66	Q8EH66 shewanella
6	30	90.9	333	2 Q89ML3	Q89ML3 bradyrhizob
7	30	90.9	360	2 Q8UHF5	Q8UHF5 agrobacteri
8	30	90.9	460	2 Q7JPK1	Q7JPK1 dictyosteli
9	30	90.9	540	1 SYFB SULMO	SYFB SULMO
10	30	90.9	569	2 Q52305	Q52305 synechococ
11	30	90.9	877	2 Q23853	Q23853 dictyosteli
12	30	90.9	1100	1 JAK3 RAT	JAK3 RAT
13	29	87.9	157	2 Q96WZ4	Q96WZ4 rattus norv
14	29	87.9	253	2 Q03093	Q03093 streptomyce
15	29	87.9	257	2 Q7P853	Q7P853 fusobacteri
16	29	87.9	312	2 Q9P162	Q9P162 campylobact
17	29	87.9	313	2 Q8RG39	Q8RG39 fusobacteri
18	29	87.9	315	1 ACCA HABIN	ACCA HABIN
19	29	87.9	315	2 Q886M7	Q886M7 pseudomonas
20	29	87.9	315	2 Q88MG4	Q88MG4 pseudomonas
21	29	87.9	316	2 Q83BJ8	Q83BJ8 coxiella bu
22	29	87.9	316	2 Q9HXZ2	Q9HXZ2 pseudomonas
23	29	87.9	317	2 Q7VPL3	Q7VPL3 haemophilus
24	29	87.9	317	2 Q8D2H6	Q8D2H6 wiggleswort
25	29	87.9	317	2 Q9CNRX9	Q9CNRX9 pasteurella
26	29	87.9	318	1 ACCA ECOLI	ACCA ECOLI
27	29	87.9	318	1 ACCA_SALTY	ACCA_SALTY
28	29	87.9	319	2 Q667KS	Q667KS yersinia
29	29	87.9	319	2 Q8PAW9	Q8PAW9 xanthomonas
30	29	87.9	319	2 Q8PMM1	Q8PMM1 xanthomonas
31	29	87.9	319	2 Q8ZH52	Q8ZH52 yersinia pe

32	29	87.9	319	2 Q7MTH6	Q7MTH6 vibrio vuln
33	29	87.9	319	2 Q7NBN1	Q7NBN1 photorhabdu
34	29	87.9	319	2 Q7VRD0	Q7VRD0 candidatus
35	29	87.9	319	2 Q87EY1	Q87EY1 xylella fas
36	29	87.9	319	2 Q87MF3	Q87MF3 vibrio para
37	29	87.9	319	2 Q8DBE5	Q8DBE5 vibrio vuln
38	29	87.9	319	2 Q8FL03	Q8FL03 escherichia
39	29	87.9	319	2 Q9JRV8	Q9JRV8 neisseria m
40	29	87.9	319	2 Q9JUF0	Q9JUF0 neisseria m
41	29	87.9	319	2 Q9KPM8	Q9KPM8 vibrio chol
42	29	87.9	319	2 Q9PGU5	Q9PGU5 xylella fas
43	29	87.9	319	2 Q6D8C7	Q6D8C7 erwinia car
44	29	87.9	321	2 Q7NT71	Q7NT71 chromobact
45	29	87.9	321	2 Q7VX94	Q7VX94 bordetella
46	29	87.9	321	2 Q7W860	Q7W860 bordetella
47	29	87.9	321	2 Q7WLK8	Q7WLK8 bordetella
48	29	87.9	322	2 Q8Y075	Q8Y075 ralteconia s
49	29	87.9	322	2 Q82VP5	Q82VP5 nitrosomona
50	29	87.9	323	2 Q62UJ9	Q62UJ9 burkholderi
51	29	87.9	323	2 Q63S70	Q63S70 burkholderi
52	29	87.9	325	2 Q65U15	Q65U15 mannheimia
53	29	87.9	326	2 Q05698	Q05698 rhizobium 1
54	29	87.9	326	2 P95623	P95623 rhizobium 1
55	29	87.9	326	2 Q7BV58	Q7BV58 rhizobium 1
56	29	87.9	334	2 Q8KG09	Q8KG09 chlorobium
57	29	87.9	370	2 Q6AUV6	Q6AUV6 oryza sativ
58	29	87.9	372	2 Q7LVQ2	Q7LVQ2 ustilago ma
59	29	87.9	385	2 Q6UAT8	Q6UAT8 agrobacteri
60	29	87.9	398	2 Q13367	Q13367 ustilago ma
61	29	87.9	450	1 LAL2_HUMAN	LAL2_HUMAN
62	29	87.9	450	1 LAL2_MOUSE	LAL2_MOUSE
63	29	87.9	450	2 Q6NS14	Q6NS14 mus musculu
64	29	87.9	450	2 Q68FO9	Q68FO9 rattus norv
65	29	87.9	455	2 Q82918	Q82918 streptomyce
66	29	87.9	504	1 TLRI_DROME	TLRI_DROME
67	29	87.9	504	2 Q9VEX8	Q9VEX8
68	29	87.9	686	2 Q9R1R7	Q9R1R7 deinococcus
69	29	87.9	688	2 P90557	P90557 leishmania
70	29	87.9	763	2 Q9W3M5	Q9W3M5 dirosophila
71	29	87.9	894	2 Q6WHC2	Q6WHC2 bacterioph
72	29	87.9	962	1 IF3A_MAIZE	IF3A_MAIZE
73	29	87.9	1025	2 Q7R6B6	Q7R6B6 giardia lam
74	29	87.9	1060	2 Q69238	Q69238 bradyrhizob
75	29	87.9	1060	2 Q89XK8	Q89XK8 bradyrhizob
76	29	87.9	1099	1 PXB3_HUMAN	PXB3_HUMAN
77	28	84.8	50	2 Q86U50	Q86U50 homo sapien
78	28	84.8	99	2 Q8GEF9	Q8GEF9 erwinia amy
79	28	84.8	109	2 Q65T23	Q65T23 mannheimia
80	28	84.8	145	2 Q8EJ60	Q8EJ60 shewanella
81	28	84.8	150	1 SSPB_HABIN	SSPB_HABIN
82	28	84.8	158	2 Q9KUE4	Q9KUE4 vibrio chol
83	28	84.8	160	2 Q9CNR9	Q9CNR9 pasteurella
84	28	84.8	165	1 SSPB_ECOLI	SSPB_ECOLI
85	28	84.8	165	1 SSPB_SHFL	SSPB_SHFL
86	28	84.8	165	2 Q8FD56	Q8FD56 escherichia
87	28	84.8	166	2 Q8XGR9	Q8XGR9 salmonella
88	28	84.8	166	2 Q7CPN4	Q7CPN4 salmonella
89	28	84.8	167	2 Q6DAB4	Q6DAB4 erwinia car
90	28	84.8	169	1 NEUT_BOVIN	NEUT_BOVIN
91	28	84.8	169	1 NEUT_MOUSE	NEUT_MOUSE
92	28	84.8	169	1 NEUT_RAT	NEUT_RAT
93	28	84.8	170	1 NEUT_CANFA	NEUT_CANFA
94	28	84.8	170	1 NEUT_HUMAN	NEUT_HUMAN
95	28	84.8	171	2 Q651I2	Q651I2 yersinia pe
96	28	84.8	171	2 Q8ZB64	Q8ZB64 yersinia pe
97	28	84.8	171	2 Q7N081	Q7N081 photorhabdu
98	28	84.8	186	2 Q85011	Q85011 tetraseimis
99	28	84.8	263	2 Q69P84	Q69P84 oryza sativ
100	28	84.8	283	2 Q96ZQ1	Q96ZQ1 sulfolobus

ALIGNMENTS

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RESULT 1
Q7NF85 PRELIMINARY; PRT; 269 AA.
AC Q7NF85;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, last sequence update)
DE G113641 protein.
GN OrderedLocustNames=G113641;
OS Gloeobacter violaceus.
OC Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
NCBI_TaxID=33072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7421.
RX MEDLINE=22977040; Pubmed=14621292;
RA Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA Sasamoto S., Matanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT cyanobacterium that lacks thylakoids.";
RL DNA Res. 10:137-145(2003).
DR EMBL; AP006580; BAC91582.1; -.
KM Complete proteome.
SQ SEQUENCE 269 AA; 30697 MW; 67644AFBA107F2B CRC64;

Query Match 90.9%; Score 30; DB 2; Length 269;
Best Local Similarity 71.4%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPYPYL 8
Db 186 PARYTL 192

RESULT 2
Q96WP3 PRELIMINARY; PRT; 286 AA.
AC Q96WP3;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Urease.
GN Name=URE;
OS Archaeodetma benhamiae (Trichophyton mentagrophytes).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Orygenales; Arthrodermataceae; Arthroderma.
NCBI_TaxID=63400;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VUT-77011;
RA Kano R., Hasegawa A.;
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -1- COFACTOR: Binds 2 nickel ions per subunit (By similarity).
CC -1- SIMILARITY: Belongs to the urease family.
DR EMBL; AB069970; BAB62910.1; -.
DR HSSP; P18314; IECX.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0016151; F:nickel ion binding; IEA.
DR GO; GO:0009039; F:urease activity; IEA.
DR GO; GO:0006807; P:nitrogen metabolism; IEA.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR005848; Urease_alpha.
DR Pfam; PF01979; Amidohydro_1; 1.
DR PRINTS; PRO1752; UREASE. 1.
DR PROSITE; PS00145; UREASE_2; 1.
KM Hydrolase; Metal-binding; Nickel.
SQ SEQUENCE 286 AA; 31471 MW; AFDD90EA7BCBE9A7 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 286;

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Best Local Similarity 71.4%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPYPYL 8
Db 21 PSRPYTL 27

RESULT 3
P95666 PRELIMINARY; PRT; 295 AA.
ID P95666
AC P95666;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, last annotation update)
DE ORP3.
GN Name=orf3;
OS Rhizobium leguminosarum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
NCBI_TaxID=384;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95383716; Pubmed=7655066;
RA Michels J., Pelemans H., Vlassak K., Verreth C., Vanderleyden J.;
RT "Identification and characterization of a Rhizobium leguminosarum bv.
RT phaseoli gene that is important for nodulation competitiveness and
RT shows structural homology to a Rhizobium fredii host-inducible gene.";
RL Mol. Plant Microbe Interact. 8:468-472(1995).
DR EMBL; S80066; ABA47010.1; -.
SQ SEQUENCE 295 AA; 33401 MW; 1C3B0A9B0DC620A CRC64;

Query Match 90.9%; Score 30; DB 2; Length 295;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPYPYL 8
Db 54 PTPPYSL 60

RESULT 4
Q98KT4 PRELIMINARY; PRT; 320 AA.
ID Q98KT4
AC Q98KT4;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, last annotation update)
DE Probable transcriptional regulator.
GN OrderedLocustNames=mlr1331;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; Pubmed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Matanabe A., Idesawa K., Ishikawa K., Kohara M., Matsuno A.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP002997; BAB48730.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0003700; F:transcription factor activity; IEA.
DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
DR InterPro; IPR009057; Homeodomain_like.
DR InterPro; IPR000005; HTHARAC.
DR InterPro; IPR011051; RmlC_like_cupin.

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DR Pfam; PF00165; HTH_ARAC; 2.
 DR PRINTS; PR00032; HTHARAC.
 DR SMART; SM00342; HTH_ARAC; 1.
 DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
 KW Complete proteome; DNA-binding; Transcription;
 KW Transcription regulation.
 SQ SEQUENCE 320 AA; 35277 MW; 0A2C56BDB6C3ED2B CRC64;

Query Match 90.9%; Score 30; DB 2; Length 320;
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
 Db 32 PRRPYXL 38

RESULT 5
 Q8EH66 PRELIMINARY; PRT; 325 AA.
 AC Q8EH66;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DE Iron-sulfur cluster-binding protein.
 GN OrderedLocustNames=SO1364;
 OS Shewanella oneidensis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 OC Shewanellaceae; Shewanella.
 NCBI_TaxID=70863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MR-1;
 RX MEDLINE=22297666; PubMed=12368813; DOI=10.1038/nbt749;
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
 RA Clayton R.A., Meyer T., Taapin A., Scott J., Beaman M.J.,
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
 RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
 RA White O., Wolf A.M., Vamathevan J.U., Weidman J.F., Impriali M.,
 RA Lee K., Berry K.J., Lee C., Mueller J., Khoult H.M., Gill J.,
 RA Utechtack T.R., McDonald L.A., Feldblum T.V., Smith H.O.,
 RA Venter J.C., Nealeon K.H., Fraser C.M.,
 RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT Shewanella oneidensis";
 RL Nat. Biotechnol. 20:1118-1123(2002).
 DR EMBL; AE015580; AAN54429.1; -.
 DR HSSP; P00246; 4FXC.
 DR TIGR; SO1364; -.
 DR GO; GO:0005489; F:electron transporter activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0006118; F:electron transport; IEA.
 DR InterPro; IPR006058; 2Fe2S_fld_BS.
 DR InterPro; IPR001834; Cyt_B5_reductase.
 DR InterPro; IPR008333; FAD binding_6.
 DR InterPro; IPR001041; Ferredoxin.
 DR InterPro; IPR001709; FPN_cyt_redctse.
 DR InterPro; IPR001433; Oxred_FAD/NAD(P).
 DR Pfam; PF00970; FAD_binding_6; 1.
 DR Pfam; PF00111; Fer2; 1.
 DR Pfam; PF00175; NAD binding_1; 1.
 DR PRINTS; PR00406; CYTB5MDTASE.
 DR PRINTS; PR00371; FPNCR.
 DR PROSITE; PS00197; 2FE2S_FERREDOXIN; 1.
 DR 2Fe-2S; Complete proteome; Iron; Iron-sulfur; Metal-binding.
 SQ SEQUENCE 325 AA; 35846 MW; EA7CAE07713C738E CRC64;

Query Match 90.9%; Score 30; DB 2; Length 325;
 Best Local Similarity 71.4%; Pred. No. 2.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 2 PRRPYXL 8
 Db 32 PRRPYXL 38

Db 32 PRRPYXL 38

RESULT 6

Q89ML3 PRELIMINARY; PRT; 333 AA.
 AC Q89ML3;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Transcriptional regulatory protein.
 GN OrderedLocustNames=D114180;
 OS Bradyrhizobium japonicum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Bradyrhizobiaceae; Bradyrhizobium.
 NCBI_TaxID=375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=USDA110;
 RX MEDLINE=22484998; PubMed=12597275;
 RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
 RA Sasamoto S., Watanabe A., Idesawa K., Iriuchih M., Kawashima K.,
 RA Kohara M., Matsumoto M., Shimp S., Tsuruoka H., Wada T., Yamada M.,
 RA Tabata S.;
 RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 RT Bradyrhizobium japonicum USDA110.";
 RL DNA Res. 9:189-197(2002).
 DR EMBL; AP005950; BAC49445.1; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0003700; F:transcription factor activity; IEA.
 DR GO; GO:0006355; F:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR003313; Arac binding.
 DR InterPro; IPR009057; Homeodomain_like.
 DR InterPro; IPR000005; HTHARAC.
 DR Pfam; PF00165; HTH_ARAC; 2.
 DR PRINTS; PR00032; HTHARAC.
 DR SMART; SM00342; HTH_ARAC; 1.
 DR PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
 KW Complete proteome; DNA-binding; Transcription;
 KW Transcription regulation.
 SQ SEQUENCE 333 AA; 37212 MW; 1B3294E40FB8F038 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 333;
 Best Local Similarity 71.4%; Pred. No. 2.9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
 Db 45 PRRPYXL 51

RESULT 7

Q8UHFS PRELIMINARY; PRT; 360 AA.
 AC Q8UHFS; Q7D079;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 23-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE Ferredoxin I (AGR_C1321p).
 GN OrderedLocustNames=AGR_C1321; AtU0727;
 OS Arabidopsis thaliana (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dupont;
 RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
 RA Wood D.W., Seubal J.C., Kaul R., Monks D.E., Kitaajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F.Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D., Str.,
 RA Chapman P., Clendinning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmeri A.,

RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*
 RT C58."

RT Science 294:2317-2323 (2001).
 RP [2]
 RP SEQUENCE FROM N.A.

RC STRAIN=Cereon;
 RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
 RA Goodner B., Hinkle G., Gatlung S., Miller N., Blanchard M.,
 RA Quorillo B., Goldman B.S., Cao Y., Akenazi M., Halling C., Mullin L.,
 RA Hummel K., Gordon J., Vaubin M., Iatchouk O., Bop A., Liu F.,
 RA Molian C., Allinger M., Doughty D., Scott C., Iappas C., Markelz B.,
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT *Agrobacterium tumefaciens* C58."

RT Science 294:2323-2328(2001).
 RL EMBL: A6009041; AAI41743.1; -
 DR EMBL: A6008007; AAK8637.1; -
 DR PIR: A12665; A12665.
 DR PIR: H97447; H97447.
 DR HSP: P00216; IEOZ.
 DR GO: GO:0005489; F:electron transporter activity; IEA.
 DR GO: GO:0016491; F:oxidoreductase activity; IEA.
 DR GO: GO:0006118; F:electron transport; IEA.
 DR InterPro: IPR006058; 2Fe2S fd BS.
 DR InterPro: IPR008333; FAD binding_6.
 DR InterPro: IPR001041; Ferredoxin.
 DR InterPro: IPR001709; FPN cvt redctse.
 DR InterPro: IPR001433; Oxred_FAD/NAD(P).
 DR InterPro: IPR001221; Phe hydroxylase.
 DR Pfam: PF00970; FAD binding_6; 1.
 DR Pfam: PF00111; Fer2; 1.
 DR Pfam: PF00175; NAD binding_1; 1.
 DR PRINTS: PR00371; FPNCR
 DR PRINTS: PR00410; PHEHYDROXILASE
 DR PROSITE: PS00197; 2FE2S_FERREDOXIN; 1.
 DR 2Fe-2S; Iron; Iron-sulfur; Metal-binding; Complete proteome.
 SQ SEQUENCE 360 AA; 39604 MW; 4EEFF7493EB50BA0 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 360;
 Best Local Similarity 71.4%; Pred. No. 3.2e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPYXL 8
 DB 77 PSRPTL 83

RESULT 8
 Q7JPK1 PRELIMINARY; PRT; 460 AA.
 AC Q7JPK1; 05-JUL-2004 (TRENBLUREL. 27, Created)
 DT 05-JUL-2004 (TRENBLUREL. 27, Last sequence update)
 DT 05-JUL-2004 (TRENBLUREL. 27, Last annotation update)
 DE Hypothetical protein.
 OS Dictyostelium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
 OX NCBI_TaxID=44689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91002566; PubMed=1976383;
 RA Giorda R., Ohmachi T., Shaw D.R., Emnis H.L.;
 RT "A shared internal threonine-glutamic acid-threonine-proline repeat
 RT defines a family of Dictyostelium discoideum spore germination
 RT specific proteins."
 RT Biochemistry 29:7264-7269(1990).

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Ax3;
 RA Giorda R., Ohmachi T., Shaw D.R., Emnis H.L.;
 RT Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U20661; AAB54078.1; -
 DR DictyBase; DDB0187057; gene.
 DR InterPro: IPR008999; Actin_crosslink.
 KW Hypothetical protein.
 SQ SEQUENCE 460 AA; 51264 MW; 799492509ACC66F6 CRC64;

Query Match 90.9%; Score 30; DB 2; Length 460;
 Best Local Similarity 71.4%; Pred. No. 4.2e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPYXL 8
 DB 72 PSRPTL 78

RESULT 9
 SYFB_SULTO STANDARD; PRT; 540 AA.
 ID SYFB_SULTO
 AC Q971D6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Phenylalanyl-tRNA synthetase beta chain (BC 6.1.1.20) (Phenylalanine--
 DE tRNA ligase beta chain) (PheRS)
 GN Name=Pherf; OrderedAccession=ST1415;
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=111955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JCM 10545 / 7;
 RX MEDLINE=21456156; PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,
 RA Sekine M., Baba S.-I., Anka A., Kosegi H., Hosoyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki U., Kushida N., Oguchi A.,
 RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yanagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermacidophilic
 RT Crenarchaeon, *Sulfolobus tokodaii* strain7."
 RT DNA Res. 8:123-140(2001).
 RL DNA Res. 8:123-140(2001).
 CC -1- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +
 CC diphosphate + L-phenylalanyl-tRNA(Phe).
 CC -1- SUBUNIT: Tetramer of two alpha and two beta chains (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain
 CC family. Subfamily 2.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL: AP000986; BAB66482.1; -
 DR HANAB; MF_00284; -; 1.
 DR InterPro: IPR005146; B3_4.
 DR InterPro: IPR005147; B5.
 DR InterPro: IPR004531; PheT arch.
 DR InterPro: IPR009061; Putativ_DNA_bind.
 DR Pfam: PF03483; B3_4; 1.
 DR Pfam: PF03484; B5; 1.
 DR TIGRFAMs; TIGR00471; PheT arch; 1.
 KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;

KW Protein biosynthesis.
SQ SEQUENCE 540 AA; 61519 MW; 956A5E8A4A923E43 CRC64;
Query Match 90.9%; Score 30; DB 1; Length 540;
Best Local Similarity 71.4%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PRRPYXL 8
DB 90 PSRRPYL 96
RESULT 10
ID 052305 PRELIMINARY; PRT; 569 AA.
AC 052305;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)
DE 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Urease alpha subunit.
GN Name=urec;
OS Synecococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32049;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7002;
RX MEDLINE=98320571; PubMed=9647800;
RA Sakamoto T., Delgailzo V.B., Bryant D.A.;
RT "Growth on urea can trigger death and peroxidation of the
cyanobacterium Synecococcus sp. strain PCC 7002.",
RL Appl. Environ. Microbiol. 64:2361-2366(1998).
CC -1- CATALYTIC ACTIVITY: Urea + H(2)O = CO(2) + 2 NH(3).
CC -1- COFACTOR: Binds 2 nickel ions per subunit (By similarity).
CC -1- SIMILARITY: Belongs to the urease family.
DR EMBL; AF035751; AAC26155.1; -.
DR HSSP; P18314; 1EXJ.
DR GO; GO:0016787; F:hydrolyase activity; IEA.
DR GO; GO:0016151; F:nickel ion binding; IEA.
DR GO; GO:0009039; F:urease activity; IEA.
DR GO; GO:0006807; P:nitrogen metabolism; IEA.
DR InterPro; IPR006680; Amidohydro. 1.
DR InterPro; IPR011059; Metallo hydrolyase.
DR InterPro; IPR005848; Urease alpha.
DR InterPro; IPR008295; Urease_alphalone.
DR Pfam; PF01979; Amidohydro_1; 1.
DR PIRSF; PIRSF001226; Urease_alpha; 1.
DR PRINTS; PR01752; UREASE.
DR TIGRFAMs; TIGR01792; urease_alph; 1.
DR PROSITE; PS01120; UREASE_1; 1.
DR PROSITE; PS00145; UREASE_2; 1.
KW Hydrolyase; Metal-binding; Nickel.
SQ SEQUENCE 569 AA; 61820 MW; DB717CASEB1642A93 CRC64;
Query Match 90.9%; Score 30; DB 2; Length 569;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PRRPYXL 8
DB 302 PTRPYTL 308
RESULT 11
ID 023853 PRELIMINARY; PRT; 877 AA.
AC 023853;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.

OX NCBI_TaxID=44689;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RX MEDLINE=91002566; PubMed=1976383;
RA Giorda R., Omachi T., Shaw D.R., Ennis H.L.;
RT "A shared internal threonine-glutamic acid-threonine-proline repeat
defines a family of Dictyostelium discoideum spore germination
specific proteins.",
RL Biochemistry 29:7264-7269(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=AX3;
RA Giorda R., Omachi T., Shaw D.R., Ennis H.L.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U20661; AAB54079.1; -.
DR DictyBase; DDB0187057; gene.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004672; F:protein kinase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 877 AA; 98709 MW; ECDB726FB1CA66CB CRC64;
Query Match 90.9%; Score 30; DB 2; Length 877;
Best Local Similarity 71.4%; Pred. No. 8.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PRRPYXL 8
DB 489 PSRRPYL 495
RESULT 12
ID JAK3 RAT STANDARD; PRT; 1100 AA.
AC 063272;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tyrosine-protein kinase JAK3 (EC 2.7.1.112) (JAK-3).
GN Name=JAK3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=94192816; PubMed=8143863; DOI=10.1016/0014-5793(94)80485-0;
RA Takahashi T., Shirasawa T.;
RT "Molecular cloning of rat JAK3, a novel member of the JAK family of
protein tyrosine kinases.",
RL FEBS Lett. 342:124-128(1994).
CC -1- FUNCTION: Tyrosine kinase of the non-receptor type, involved in
the interleukin-2 and interleukin-4 signaling pathway.
CC Phosphorylates STAT6, IRS1, IRS2 and PI3K.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Wholly intracellular, possibly membrane
associated (By similarity).
CC -1- TISSUE SPECIFICITY: Transcribed in a variety of tissues including
spleen, lung, kidney and intestine.
CC -1- DOMAIN: Possesses two phosphotransferase domains. The second one
probably contains the catalytic domain (By similarity), while the
presence of slight differences suggest a different role for domain
1.
CC -1- PTM: Tyrosine phosphorylated in response to IL-2 and IL-4 (By
similarity).
CC -1- SIMILARITY: Belongs to the Tyr protein kinase family. JAK
subfamily.
CC -1- SIMILARITY: Contains 1 FERM domain.

CC -1- SIMILARITY: Contains 1 SH2 domain.
 CC -----
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DR EMBL: D28508; BA05868.1; -.
 DR PIR: S43577; S43577.
 DR HSSP: P11362; IFGK.
 DR RGD: 2940; Jak3.
 DR InterPro: IPR000299; Band_4.1.
 DR InterPro: IPR009127; JAK.
 DR InterPro: IPR009130; JAK.
 DR InterPro: IPR011009; Kinase_like.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001245; Tyr_Kinase.
 DR InterPro: IPR008266; Tyr_Kinase_AS.
 DR Pfam: PF00069; Kinase_2.
 DR PRINTS: PR01823; JANUSKINASE.
 DR PRINTS: PR01826; JANUSKINASE3.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Prot_Kinase; 2.
 DR ProDom: PD000093; SH2_1.
 DR SMART: SM00285; B41; 1.
 DR SMART: SM00282; SH2; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS00660; FERM_1; FALSE_NEG.
 DR PROSITE: PS00661; FERM_2; FALSE_NEG.
 DR PROSITE: PS00657; FERM_3; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 2.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS00001; SH2; FALSE_NEG.
 DR ATP-binding; Phosphorylation; Repeat; SH2 domain; Transferase;
 KW Tyrosine-protein kinase.
 FT DOMAIN 24 353 FERM.
 FT DOMAIN 372 472 SH2 (atypical).
 FT DOMAIN 517 777 Protein kinase 1.
 FT DOMAIN 818 1091 Protein kinase 2.
 FT NP_BIND 824 832 ATP (By similarity).
 FT BINDING 851 851 ATP (By similarity).
 FT ACT_SITE 945 945 Proton acceptor (By similarity).
 FT MOD_RES 976 976 Phosphotyrosine (by autocatalysis) (By
 similarity).
 SQ SEQUENCE 1100 AA; 122560 MW; 1D59CA05F4DD7EE2 CRC64;

Query March 90.9%; Score 30; DB 1; Length 1100;
 Best Local Similarity 71.4%; Pred. No. 1.1e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPXYL 8
 Db 228 PSRYAL 234

RESULT 13
 Q96M24 PRELIMINARY; PRT; 157 AA.
 AC Q96M24;
 DT 01-DEC-2001 (TrEMBLrel. 19; Created)
 DT 01-DEC-2001 (TrEMBLrel. 19; Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28; Last annotation update)
 DE Hypothetical protein FLJ31659.
 GN Name=FLJ31659;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OC NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.
 RX PubMed=14702039; DOI=10.1038/ng1285;
 RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
 RA Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
 RA Sekine M., Ohtsuka M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
 RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
 RA Hirakawa K., Saeta K., Iwayanagi T., Wagatsuma M., Shiratori K.,
 RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
 RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
 RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
 RA Ninomiya K., Iwibashi T., Yamashita H., Murakawa K., Fujimori K.,
 RA Tanai H., Kimura M., Watanabe M., Hirakawa S., Chiba Y., Iwida S.,
 RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Houta T., Kusano J.,
 RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
 RA Masashiro K., Yuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shibahara T., Sano S.,
 RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiyara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Ohtani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senda T.,
 RA Matsunura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
 RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
 RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Maeno H., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 cDNAs.";
 RL Nat. Genet. 36:40-45(2004).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603999;
 RA Strauberg R.L., Feigold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Sherman C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.M., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,
 RA Diachenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C.,
 RA Brownstein M.J., Udell T.B., Toshitsuki S., Caranci P., Prange C.,
 RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarene P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schenck A., Schein J.E.,
 RA Jones S.V., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Prostate;
 RA Strauberg R.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK056221; BAB7123.1; -.
 DR EMBL: BC022381; AAH22381.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 157 AA; 17021 MW; 7DA9AE4F963BDF56 CRC64;

Query March 87.9%; Score 29; DB 2; Length 157;
 Best Local Similarity 71.4%; Pred. No. 2e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPXYL 8

Db 43 PNRPYTL 49

RESULT 14

ID 003093 PRELIMINARY; PRT; 253 AA.
AC 003093;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Thioesterase
OS Streptomyces hygroscopicus
OC Bacteria; Actinobacteria; Actinobacteriales; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1912;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91294191; PubMed=2066341;
RA Raibaud A., Zalcman M., Holt T.G., Tizard R., Thompson C.J.;
RT "Nucleotide sequence analysis reveals linked N-acetyl hydrolase, thioesterase, transport, and regulatory genes encoded by the bialaphos biosynthetic gene cluster of Streptomyces hygroscopicus.";
RL J. Bacteriol. 173:4454-4463(1991).
DR EMBL; M64783; AAA79278.1; -.
DR PIR; C47031; C47031.
DR GO; GO:0016788; F:hydrolase activity, acting on ester bonds; IEA.
DR GO; GO:0009058; P:biosynthesis; IEA.
SQ SEQUENCE 253 AA; 27630 MW; 26602CDD0DEC2A3 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 253;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPXYL 8
Db 78 PDRPYL 84

RESULT 15

ID 07P853 PRELIMINARY; PRT; 257 AA.
AC 07P853;
DT 01-MAR-2004 (TREMblrel. 26, Created)
DT 01-MAR-2004 (TREMblrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMblrel. 26, Last annotation update)
DE Acetyl-coenzyme A carboxylase subunit alpha (EC 6.4.1.2).
GN Name=FNV2185;
OS Fusobacterium nucleatum subsp. vincentii ATCC 49256.
OC Bacteria; Fusobacteriales; Fusobacteriaceae;
OC Fusobacterium.
OX NCBI_TaxID=209882;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 49256;
RA Karpman V., Ivanova N., Anderson I., Reznik G., Bhattacharya A., Haselkorn R., Overbeek R., Kyrides N., D'Souza M., Walunas T., Submitted (JUN-2003) to the EMBL/Genbank/DBJ databases.
RL -1- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL; AAB01000005; EAA25081.1; -.
DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR001095; Ac-CoA_carboxylA.
DR Pfam; PF03255; ACCA; 1.
DR PRINTS; PRO1069; ACCCTRFRASEA.
DR TIGRfams; TIGR00513; acca; 1.

KW Ligase; Transferase.
SQ SEQUENCE 257 AA; 28515 MW; ABC42E7A2D95C319 CRC64;
Query Match 87.9%; Score 29; DB 2; Length 257;
Best Local Similarity 71.4%; Pred. No. 3.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPXYL 8
Db 6 PDRPYL 12

RESULT 16

ID 09P162 PRELIMINARY; PRT; 312 AA.
AC 09P162;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Acetyl-coenzyme A carboxylase subunit alpha (EC 6.4.1.2).
GN Name=acca; OrderedLocustNames=Cj0443;
OS Campylobacter jejuni.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales; Campylobacteraceae; Campylobacter.
OX NCBI_TaxID=197;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 11168;
RX MEDLINE=20150912; PubMed=10688204; DOI=10.1038/35001088;
RA Parkhill J., Wren B.W., Mungall K.L., Kettle J.M., Churcher C.M., Baahm D., Chillingworth T., Davies R.M., Felwell T., Holtroyd S., Jasele K., Karlyshav A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M., Whitehead S., Barrett B.G.;
RT "The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypervariable sequences.";
RL Nature 403:665-668(2000).
DR EMBL; AL139075; CAB74279.1; -.
DR PIR; A81389; A81389.

DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR001095; Ac-CoA_carboxylA.
DR Pfam; PF03255; ACCA; 1.
DR PRINTS; PRO1069; ACCCTRFRASEA.
DR TIGRfams; TIGR00513; acca; 1.
KW Complete proteome; Ligase; Transferase.
SQ SEQUENCE 312 AA; 34253 MW; 8DD611C042DADA4 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 312;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPXYL 8
Db 60 PDRPYL 66

RESULT 17

ID 08RG99 PRELIMINARY; PRT; 313 AA.
AC 08RG99;
DT 01-JUN-2002 (TREMblrel. 21, Created)
DT 01-JUN-2002 (TREMblrel. 21, Last sequence update)
DT 01-JUN-2003 (TREMblrel. 24, Last annotation update)
DE Acetyl-coenzyme A carboxylase subunit alpha (EC 6.4.1.2).
GN OrderedLocustNames=FN0409;
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteriales; Fusobacteriaceae;

CC Fusobacterium.
 OX NCBI_TaxID=76856;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=21886394; PubMed=11889109;
 RX DOI=10.1128/JB.184.7.2005-2018.2002;
 RA Kaparakal V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L.,
 RA Vasileva O., Chu L., Kogan Y., Chaga O., Goldsman E., Bernal A.,
 RA Larsen N., D'Souza M., Malunas T., Pusch G., Haselkorn R.,
 RA Fongseim M., Kyriades N.C., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 RT nucleatum strain ATCC 25586.";
 RL J. Bacteriol. 184:2005-2018(2002).
 DR EMBL: AE010552; AAL94612.1;
 DR GO: GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO: GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO: GO:0016749; F:ligase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro: IPR01095; Ac-CoA_carboxylA.
 DR Pfam: PF03255; ACQA; 1
 DR PRINTS; PRO1069; ACCCTFRPASEA.
 DR TIGRFAMs; TIGR00513; acqa; 1.
 DR Complete proteome; Ligase; Transferase.
 KM SEQUENCE 313 AA; 35303 MW; 878CFBC3F8D261 CRC64;
 SQ

Query Match 87.9%; Score 29; DB 2; Length 313;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
 Db 62 PRRPYTL 68

RESULT 18
 ACQA_HAEIN STANDARD; PRT; 315 AA.
 ID ACQA_HAEIN STANDARD; PRT; 315 AA.
 AC P43872;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
 DE [EC 6.4.1.2].
 GN Name=acqa; OrderedLocusNames=HI0406;
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / KM20 / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
 RA McElwaine K., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA Klenzmann J., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shiley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
 RA Fine L.D., Fitchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).
 CC -1- FUNCTION: This protein is a component of the acetyl coenzyme A
 CC carboxylase complex; first, biotin carboxylase catalyzes the
 CC carboxylation of the carrier protein and then the transcarboxylase
 CC transfers the carboxyl group to form malonyl-CoA (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
 CC + malonyl-CoA.

CC -1- PATHWAY: long-chain fatty acid biosynthesis; first step.
 CC -1- SUBUNIT: Acetyl-CoA carboxylase is a heterohexamer of biotin
 CC carboxyl carrier protein, biotin carboxylase and the two subunits
 CC of carboxyl transferase in a 2:2 complex (By similarity).
 CC -1- SIMILARITY: Belongs to the acqa family.
 CC -1- SIMILARITY: Contains 1 acetyl-coenzyme A carboxyltransferase Cter
 CC domain.

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DR EMBL: U33724; AAC22065.1;
 DR PIR: I64065; I64065.
 DR TIGR: HI0406;
 DR InterPro: IPR001095; Ac-CoA_carboxylA.
 DR Pfam: PF03255; ACQA; 1.
 DR PRINTS; PRO1069; ACCCTFRPASEA.
 DR TIGRFAMs; TIGR00513; acqa; 1.
 DR PROSITE; PS50989; COA_CT_CTER; 1.
 DR Complete proteome; Fatty acid biosynthesis; Ligase.
 KM SEQUENCE 315 AA; 35126 MW; E3B0B498A2686B23 CRC64;
 SQ

Query Match 87.9%; Score 29; DB 1; Length 315;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
 Db 66 PRRPYTL 72

RESULT 19
 Q886M7 PRELIMINARY; PRT; 315 AA.
 ID Q886M7 PRELIMINARY; PRT; 315 AA.
 AC Q886M7;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Acetyl-CoA carboxylase, carboxyl transferase, alpha subunit.
 GN Name=acqa; OrderedLocusNames=PSPT01550;
 OS Pseudomonas syringae (pv. tomato).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=323;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DC3000;
 RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
 RA Buell C.R., Joardar V., Lindeberg M., Selengut U., Paulsen I.T.,
 RA Gwin M.L., Dodson R.U., DeBoy R.T., Durkin A.S., Kolony J.F.,
 RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
 RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu Q.,
 RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
 RA Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
 RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
 RA Bender C.L., White O., Fraser C.M., Collier A.;
 RA "The complete genome sequence of the Arabidopsis and tomato pathogen
 RT Pseudomonas syringae pv. tomato DC3000."
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
 DR EMBL: AE016661; AAO55070.1;
 DR TIGR: PSPT01550;
 DR GO: GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO: GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO: GO:0016740; F:transferase activity; IEA.
 DR GO: GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro: IPR01095; Ac-CoA_carboxylA.
 DR Pfam; PF03255; ACQA; 1.

DR PRINTS; PRO1069; ACCCTFRPASEA.
DR TIGRFAMs; TIGR00513; accA; 1.
KM Complete proteome; Transferase.
SQ SEQUENCE 315 AA; 34975 MW; A878C54C71D5C555 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 315;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPYPYL 8
Db 67 PRRPYTL 73

RESULT 20
Q88MG4 PRELIMINARY; PRT; 315 AA.
ID Q88MG4;
AC Q88MG4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Acetyl-CoA carboxylase, carboxyl transferase, alpha subunit.
GN Name=acca; OrderedLocustNames=PP1607;
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
NCBI_TaxID=160488;
RX MEDLINE=22423060; PubMed=12534463;
RA Neilson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., Deboy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouli H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzar A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Medler H., Lauber J., Stjepandic D., Hohnselt J., Straetz M., Heim S.,
RA Kiewitz C., Eissen J.A., Timmis K.N., Duesterhoeft A., Tuenmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AB016779; AA067228.1; -.
DR TIGR; PP1607; -.
DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR01095; Ac-CoA_carboxylA.
DR InterPro; IPR010982; Lambda_like_DNA.
DR Pfam; PF03255; ACCA; 1.
DR PRINTS; PRO1069; ACCCTFRPASEA.
DR TIGRFAMs; TIGR00513; accA; 1.
KM Complete proteome.
SQ SEQUENCE 315 AA; 35135 MW; 65952AE13959EDAD CRC64;

Query Match 87.9%; Score 29; DB 2; Length 315;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPYPYL 8
Db 67 PRRPYTL 73

RESULT 21
Q83BJ8 PRELIMINARY; PRT; 316 AA.
ID Q83BJ8;
AC Q83BJ8;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Acetyl-CoA carboxylase, carboxyl transferase, alpha subunit.
GN Name=acca; OrderedLocustNames=CBU1510;

OS Coxiella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OX NCBI_TaxID=777;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nine Mile phase I / R84 493;
RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
RA Seahardt R., Paulsen I.T., Eissen J.A., Read T.D., Neilson K.E.,
RA Nelson W.C., Ward N.L., Tettelin H., Davidson T.M., Beanan M.J.,
RA Deboy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.O.,
RA Khouli H.M., Lee K.H., Carly H.A., Scanlan D., Heinzen R.A.,
RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
RT "Complete genome sequence of the Q-fever pathogen, Coxiella
RT burnetii.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
DR EMBL; AB016964; AA091007.1; -.
DR TIGR; CBU1510; -.
DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR01095; Ac-CoA_carboxylA.
DR InterPro; IPR010982; Lambda_like_DNA.
DR Pfam; PF03255; ACCA; 1.
DR PRINTS; PRO1069; ACCCTFRPASEA.
DR TIGRFAMs; TIGR00513; accA; 1.
KM Complete proteome; Transferase.
SQ SEQUENCE 316 AA; 35377 MW; 47A945854312DA45 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 316;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPYPYL 8
Db 67 PLRYPYL 73

RESULT 22
Q9HXZ2 PRELIMINARY; PRT; 316 AA.
ID Q9HXZ2;
AC Q9HXZ2;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Acetyl-coenzyme A carboxyl transferase (alpha
DE subunit).
GN Name=acca; OrderedLocustNames=PA3639;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
RA Gardner R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Mong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
DR EMBL; AB004783; AAC07027.1; -.
DR PIR; D83192; D83192.
DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR01095; Ac-CoA_carboxylA.

DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCTFRASEA.
 DR TIGRFAMs; TIGR00513; acca; 1.
 KM Complete proteome; Transferase.
 SQ SEQUENCE 316 AA; 34947 MW; 91409418A79FB484 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 316;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
 Db 67 PRRPYTL 73

RESULT 23

Q7VPL3 PRELIMINARY; PRT; 317 AA.

AC Q7VPL3; 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Acetyl-CoA carboxylase carboxyl transferase subunit alpha.
 GN Name=acca; OrderedLocNames=HD0051;
 OS Haemophilus ducreyi.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Haemophilus.
 OX NCBI_TaxID=730;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=3500HP / ATCC 700724;
 RA Munson R.S. Jr., Ray W.C., Manaitas G., Sabo P., Mungur R.,
 RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.;
 RT "The complete genome sequence of Haemophilus ducreyi."
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AEO17151; AAP5066.1; -
 DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro: IPR001095; Ac-CoA carboxylA.
 DR InterPro: IPR010982; Lambda_like_DNA.
 DR Pfam; PF03255; ACCA; 1.
 DR TIGRFAMs; TIGR00513; acca; 1.
 KM Complete proteome; Transferase.
 SQ SEQUENCE 317 AA; 35212 MW; 3DFB30A76808796C CRC64;

Query Match 87.9%; Score 29; DB 2; Length 317;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
 Db 68 PRRPYTL 74

RESULT 24

Q8DZH6 PRELIMINARY; PRT; 317 AA.

AC Q8DZH6; 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE AccA protein.
 GN Name=acca; OrderedLocNames=MIGR3780;
 OS Wigglesworthia glossinidia brevipalpis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Wigglesworthia.
 OX NCBI_TaxID=36870;
 RN [1]

RP SEQUENCE FROM N.A.
 RC MEDLINE=22297718; PubMed=12219091; DOI=10.1038/ng986;
 RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,

RA Aksoy S.;
 RT "Genome sequence of the endocellular obligate symbiont of tsetse
 RT files, Wigglesworthia glossinidia."
 RL Nat. Genet. 32:402-407(2002).
 DR EMBL; AB063522; BAC24524.1; -
 DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro: IPR001095; Ac-CoA carboxylA.
 DR InterPro: IPR010982; Lambda_like_DNA.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCTFRASEA.
 DR TIGRFAMs; TIGR00513; acca; 1.
 KM Complete proteome.
 SQ SEQUENCE 317 AA; 35637 MW; 26586C43A815091B CRC64;

Query Match 87.9%; Score 29; DB 2; Length 317;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
 Db 68 PRRPYAL 74

RESULT 25

Q9CNX9 PRELIMINARY; PRT; 317 AA.

AC Q9CNX9; 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE AccA.
 GN Name=acca; OrderedLocNames=PM0292;
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN=Pm70;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;
 RT "Complete genomic sequence of Pasteurella multocida Pm70."
 RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 DR EMBL; AEO06064; AK02376.1; -
 DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro: IPR001095; Ac-CoA carboxylA.
 DR InterPro: IPR00577; FGGY_Kin.
 DR InterPro: IPR010982; Lambda_like_DNA.
 DR Pfam; PF03255; ACCA; 1.
 DR PRINTS; PR01069; ACCCTFRASEA.
 DR TIGRFAMs; TIGR00513; acca; 1.
 DR PROSITE; PS00445; FGGY_KINASES_2; UNKNOWN_1.
 KM Complete proteome.
 SQ SEQUENCE 317 AA; 35341 MW; F8B3DDA93723D1D6 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 317;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
 Db 68 PRRPYTL 74

RESULT 26

ACCA_ECOLI STANDARD; PRT; 318 AA.

AC P30867; 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, last sequence update)
 DE 25-JAN-2005 (Rel. 46, last annotation update)
 DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
 DE (EC 6.4.1.2)
 GN Name=ccaA; OrderedLocNames=b0185, z0197, EC60187, SF0175, S0178;
 OS Escherichia coli,
 OS Escherichia coli O157:H7, and
 OS Shigella flexneri.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562, 8334, 623;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC SPECIES=E.coli; STRAIN=K12 / W3110;
 RX MEDLINE=92380982; PubMed=1355089;
 RA Li S.-J., Cronan J.E. Jr.;
 RT "The genes encoding the two carboxyltransferase subunits of
 RT Escherichia coli acetyl-CoA carboxylase."
 RL J. Biol. Chem. 267:16841-16847(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / W3110;
 RA Yamamoto Y.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=97429617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
 RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / W3110;
 RA Yamamoto K., Mori H., Mureyama N., Kataoka K., Yano M., Itoh T.,
 RA Takemoto Y., Inokuchi H., Miki T., Hatada E., Fukuda R., Ichihara S.,
 RA Mizuno T., Makino K., Nakata A., Yura T., Sampaio G., Mizobuchi K.;
 RT "Systematic sequencing of the Escherichia coli genome: analysis of the
 RT 4.0 - 6.0 min (189,987 - 281,416bp) region."
 RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli;
 RA Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,
 RA Davis K., Federlepiel N., Hyman R., Kalman S., Komp C., Kurdi O.,
 RA Lashkari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,
 RA Davis R.W.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
 RX MEDLINE=1079533; PubMed=11206551; DOI=10.1038/35054089;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackert J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobbeck B.U., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blatner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."
 RL Nature 409:529-533(2001).
 RN [7]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=O157:H7 / Sakai / RIMD 050952 / EHEC;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,
 RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";

RL DNA Res. 8:11-22(2001).
 RN [8]
 RP SEQUENCE OF 163-318 FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / W3110;
 RX MEDLINE=97369816; PubMed=92262571;
 RA Kikuchi Y., Kojima H., Tanaka T., Takatsuka Y., Kamio Y.;
 RT "Characterization of a second lysine decarboxylase isolated from
 RT Escherichia coli."
 RL J. Bacteriol. 179:4486-4492(1997).
 RN [9]
 RP SEQUENCE OF 1-12.
 RC SPECIES=E.coli; STRAIN=K12 / EMG2;
 RX MEDLINE=22272406; PubMed=12364590; DOI=10.1093/nar/gkf566;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 RT in the genome of Escherichia coli K-12."
 RL Electrophoresis 18:1259-1313(1997).
 RN [10]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; PubMed=12364590; DOI=10.1093/nar/gkf566;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157."
 RL Nucleic Acids Res. 30:4432-4441(2002).
 RN [11]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
 RX MEDLINE=22590274; PubMed=12704152;
 RA DOI=10.1128/JAI.71.5.2775-2786.2003;
 RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
 RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
 RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
 RA Schwartz D.C., Blatner F.R.;
 RT "Complete genome sequence and comparative genomics of Shigella
 RT flexneri serotype 2a strain 2457T."
 RL Infect. Immun. 71:2775-2786(2003).
 CC -1- FUNCTION: This protein is a component of the acetyl coenzyme A
 CC carboxylase complex; first, biotin carboxylase catalyzes the
 CC carboxylation of the carrier protein and then the transcarboxylase
 CC transfers the carboxyl group to form malonyl-CoA.
 CC -1- CATALYTIC ACTIVITY: ADP + acetyl-CoA + HCO(3)(-) = ADP + phosphate
 CC + malonyl-CoA.
 CC -1- PATHWAY: Long-chain fatty acid biosynthesis; first step.
 CC -1- SUBUNIT: Acetyl-CoA carboxylase is a heterohexamer of biotin
 CC carboxyl carrier protein, biotin carboxylase and the two subunits
 CC of carboxyl transferase in a 2:2 complex.
 CC -1- SIMILARITY: Belongs to the accA family.
 CC -1- SIMILARITY: Contains 1 acetyl-coenzyme A carboxyltransferase Cter
 CC domain.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL; M66394; AAA70370.1; -;
 DR EMBL; D49445; BAA08425.1; -;
 DR EMBL; D49445; BAA08425.1; -;
 DR EMBL; D83516; BAA77860.1; -;
 DR EMBL; D83516; BAA77860.1; -;
 DR EMBL; U70214; AAB08614.1; -;
 DR EMBL; AE005194; AAC54487.1; -;
 DR EMBL; AE002350; BAB3610.1; -;
 DR EMBL; D87518; BAA21655.1; -;
 DR EMBL; AE015054; AAN41837.1; -;
 DR EMBL; AE015054; AAN41837.1; -;
 DR EMBL; AE016978; AAP15718.1; -;

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DR PIR; A43452; A43452.
DR PIR; C85503; C85503.
DR PIR; C90652; C90652.
DR ECHOBASE; EB1600; -.
DR ECHOBASE; EB1647; acca.
DR InterPro; IPR001095; Ac-CoA carboxylA.
DR Pfam; PF03255; ACCA.1.
DR PRINTS; PRO1069; ACCCTRFRASEA.
DR TIGRFAMs; TIGR00513; acca.1.
DR PROSITE; PSS0989; COA_CT_CTER; 1.
KW Complete proteome; Direct protein sequencing; Fatty acid biosynthesis;
FT INIT MET 0 0
FT DOMAIN 83 118 Acyl-CoA-binding domain (Potential).
FT CONFLICT 24 24 V->G (in Ref. 4).
SQ SEQUENCE 318 AA; 35110 MM; 8938BE08E5D3C9AD CRC64;

Query Match 87.9%; Score 29; DB 1; Length 318;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYL 8
Db 69 PRRPYL 75

RESULT 27
ACCA_SALTY STANDARD; PRT; 318 AA.
ID ACCA_SALTY STANDARD; PRT; 318 AA.
AC P40674;
DT 01-FEB-1995 (Rel. 31, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha
   (EC 6.4.1.2).
GN Name=acca; OrderedLocNames=STM0232, STY0255, t0233;
OS Salmonella typhimurium; and
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
   Courtney L., Portolillo S., Ali J., Dante M., Du P., Hou S., Layman D.,
   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
   Waterston R., Wilson R.K.;
RA "Complete genome sequence of Salmonella enterica serovar Typhimurium
   LT2."
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE OF 1-35 FROM N.A.
RC SPECIES=S.typhimurium;
RX MEDLINE=90068797; PubMed=2676978;
RA Lancy E.D., Lifschits M.R., Munson P., Maurer R.;
RT "Nucleotide sequences of dnaP, the gene for the polymerase subunit of
   DNA polymerase III in Salmonella typhimurium, and a variant that
   facilitates growth in the absence of another polymerase subunit."
RL J. Bacteriol. 171:5581-5586(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Churchill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
   Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
   Baker S., Baaham D., Brooks K., Chillingworth T., Connerton P.,
   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
   Felwell T., Hamlin N., Haque A., Hien T.T., Holtroyd S., Jasele K.,
   Krogh A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,
   Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,

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RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
   enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RA DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
   Burland V., Kodyanski V., Schwartz D.C., Blattner F.R.;
RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
   and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: This protein is a component of the acetyl coenzyme A
   carboxylase complex; first, biotin carboxylase catalyzes the
   carboxylation of the carrier protein and then the transcarboxylase
   transfers the carboxyl group to form malonyl-CoA.
CC -1- CATALYTIC ACTIVITY: ATP + acetyl-CoA + HCO(3) (-) = ADP + phosphate
   + malonyl-CoA.
CC -1- PATHWAY: Long-chain fatty acid biosynthesis; first step.
CC -1- SUBUNIT: Acetyl-CoA carboxylase is an heterohexamer of biotin
   carboxyl carrier protein, biotin carboxylase and the two subunits
   of carboxyl transferase in a 2:2 complex.
CC -1- SIMILARITY: Belongs to the accA family.
CC -1- SIMILARITY: Contains 1 acetyl-coenzyme A carboxyltransferase Cter
   domain.
CC -----
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   or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB008705; AAI19196.1; -.
DR EMBL; M26046; -; NOT ANNOTATED_CDS.
DR EMBL; AL627266; CAD08690.1; -.
DR EMBL; AE016834; AAO67963.1; -.
DR StvGene; SG10496; acca.
DR InterPro; IPR001095; Ac-CoA_carboxylA.
DR Pfam; PF03255; ACCA.1.
DR PRINTS; PRO1069; ACCCTRFRASEA.
DR TIGRFAMs; TIGR00513; acca.1.
DR PROSITE; PSS0989; COA_CT_CTER; 1.
KW Complete proteome; Fatty acid biosynthesis; Ligase.
FT INIT MET 0
FT DOMAIN 83 118
FT CONFLICT 16 16 Acyl-CoA-binding domain (Potential).
SQ SEQUENCE 318 AA; 35212 MM; 749B990EC011F9D0 CRC64;

Query Match 87.9%; Score 29; DB 1; Length 318;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYL 8
Db 69 PRRPYL 75

RESULT 28
0667K5 PRELIMINARY; PRT; 319 AA.
ID 0667K5;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit al. . . (EC
   6.4.1.2).
GN Name=acca; ORFNames=YPRB2987;
OS Yersinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

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OC Enterobacteriaceae; Yersinia.
 OX NCBI_TaxID=273123;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IP 32953;
 RX PubMed=15358585;
 RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
 RA Regala W.M., Georgescu A.M., Verges L.M., Land M.L., Motin L.V.,
 RA Brubaker R.R., Fowler J., Hinebusch B.J., Marceau M., Medigue C.,
 RA Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M.,
 RA Derbise A., Hauser L.J., Garcia E.,
 RT "Insights into the genome evolution of Yersinia pestis through whole
 RT genome comparison with Yersinia pseudotuberculosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
 DR EMBL: BX363398; CAH22225.1;
 DR GO: GO:0016874; F:ligase activity; IEA.
 DR GO: GO:0016740; P:transferase activity; IEA.
 DR InterPro: IPR01095; Ac-CoA_carboxylA.
 DR Pfam: PF03255; ACCA; 1.
 DR PRINTS: PRO1069; ACCCTFRASEA.
 DR TIGRFAMs: TIGR00513; acca; 1.
 KM Ligase; Transferase.
 SQ SEQUENCE 319 AA; 35495 MW; 45ABBI90ECT7B402E CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 PXPPLYL 8
 Db 70 PRRPYTL 76
 RESULT 29
 ID Q8PWA9 PRELIMINARY; PRT; 319 AA.
 AC Q8PWA9;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Acetyl-coenzyme A carboxylase carboxyl transferase.
 GN Name=acca; OrderedLocNames=XCC1357;
 OS Xanthomonas campestris (pv. campestris).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=340;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 33913 / NCPPB 528;
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Camnava F., Cardozo J., Chambergo F., Clapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.";
 RL Nature 417:459-463(2002).
 DR EMBL: AEO12214; AAM40655.1;
 DR GO: GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO: GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO: GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro: IPR01095; Ac-CoA_carboxylA.

DR InterPro: IPR010982; Lambda_like_DNA.
 DR Pfam: PF03255; ACCA; 1.
 DR PRINTS: PRO1069; ACCCTFRASEA.
 DR TIGRFAMs: TIGR00513; acca; 1.
 KM Complete proteome.
 SQ SEQUENCE 319 AA; 35199 MW; 115E14A2F2DD12AC CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 PXPPLYL 8
 Db 67 PRRPYTL 73
 RESULT 30
 ID Q8PWA9 PRELIMINARY; PRT; 319 AA.
 AC Q8PWA9;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Acetyl-coenzyme A carboxylase carboxyl transferase.
 GN Name=acca; OrderedLocNames=XAC1405;
 OS Xanthomonas axonopodis (pv. citri).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xanthomonas.
 OX NCBI_TaxID=92829;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=306 / ATCC 13902 / XV 101;
 RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
 RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furlan L.R.,
 RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
 RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
 RA Camarotte G., Camnava F., Cardozo J., Chambergo F., Clapina L.P.,
 RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
 RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
 RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
 RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
 RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
 RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
 RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
 RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
 RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
 RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
 RA Setubal J.C., Kitajima J.P.;
 RT "Comparison of the genomes of two Xanthomonas pathogens with differing
 RT host specificities.";
 RL Nature 417:459-463(2002).
 DR EMBL: AEO11772; AAM36276.1;
 DR GO: GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO: GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO: GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro: IPR01095; Ac-CoA_carboxylA.
 DR InterPro: IPR010982; Lambda_like_DNA.
 DR Pfam: PF03255; ACCA; 1.
 DR PRINTS: PRO1069; ACCCTFRASEA.
 DR TIGRFAMs: TIGR00513; acca; 1.
 KM Complete proteome.
 SQ SEQUENCE 319 AA; 35270 MW; 385DBBABAEB0DC3 CRC64;
 Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Oy 2 PXPPLYL 8
 Db 67 PRRPYTL 73
 RESULT 31

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Q8ZH52          PRELIMINARY;      PRT;      319 AA.
ID Q8ZH52
AC Q8ZH52; Q74S51; Q7CH19;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC
DE 6.4.1.2) (Acetyl CoA carboxylase, carboxyltransferase component, alpha
DE subunit).
GN Name:accA; OrderedLocNames=YP2190, YP01060, YJ119;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_Taxid=632;
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RC MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holtroyd S., Jagers K., Karlyshev A.V.,
RA Leather S., Moutle S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RC MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Peterhosen J.D., Linder L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Watson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN RN
RP SEQUENCE FROM N.A.
RC STRAIN=91001 / Biovar Mediaevalis;
RC Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
RC Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
RC Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
RC Yang R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ414146; CAC89902.1; -
DR EMBL; AE013912; AAM86669.1; -
DR EMBL; AE017137; AAS62974.1; -
DR PIR; AC0130; AC0130.
DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR Pfam; PF03255; ACCA; 1
DR PRINTS; PRO1069; ACCCTFRASEA.
DR TIGRFAMs; TIGR00513; accA; 1.
KM Complete proteome; ligase; transferase.
SQ SEQUENCE 319 AA; 35495 MW; 45ABH190EC7B402E CRC64;

Query Match      87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYTL 8
DB 70 PRRPYTL 76

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ID Q7MH6          PRELIMINARY;      PRT;      319 AA.
AC Q7MH6;
DT 01-MAR-2004 (TReMBLrel. 26, Created)
DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Acetyl-CoA carboxylase alpha subunit.
GN OrderedLocNames=VY2540;
OS Bacteria; Proteobacteria (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_Taxid=196600;
RN RN
RP SEQUENCE FROM N.A.
RC PubMed=14656965; DOI=10.1101/gr.1295503;
RC Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RC Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RC Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
DR EMBL; AP005340; BAC95304.1; -
DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR001095; Ac-CoA_carboxylA.
DR Pfam; PF03255; ACCA; 1.
DR PRINTS; PRO1069; ACCCTFRASEA.
DR TIGRFAMs; TIGR00513; accA; 1.
KM Complete proteome.
SQ SEQUENCE 319 AA; 35572 MW; 25D6FDB230DC138 CRC64;

Query Match      87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYTL 8
DB 70 PRRPYTL 76

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DR TIGRFAMs; TIGR00513; acca; 1.
KM Complete proteome.
SQ SEQUENCE 319 AA; 35523 MW; E1F08BF0F450FCE2 CRC64;

Query Match
Best Local Similarity 87.9%; Score 29; DB 2; Length 319;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPPLYL 8
DB 70 PRRPYTL 76

RESULT 34
QVVRD0
ID QVVRD0 PRELIMINARY; PRT; 319 AA.
AC QVVRD0;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC
6.4.1.2).
GN Name=acca; OrderedLocuNames=Bf1287;
OS Candidatus Blochmannia floridanus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
OX NCBI_TaxID=203907;
RN [1]
SQ SEQUENCE FROM N.A.
RX MEDLINE=22784745; PubMed=12866019; DOI=10.1073/pnas.1533499100;
RA Gil R., Silva F.J., Zientz E., Delmotte F., Gonzalez-Candelas F.,
RA Latorre A., Rausell C., Kamerbeek J., Gadau J., Heidegger B.,
RA van Ham R.C.H.J., Grose R., Moya A.;
RT "The genome sequence of Blochmannia floridanus: comparative analysis
of reduced genomes.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:9388-9393 (2003).
DR EMBL; BX248585; CAD83358.1; -.
DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR01095; Ac-CoA_carboxylA.
DR Pfam; PF03255; ACCA; 1.
DR TIGRFAMs; TIGR00513; acca; 1.
KM Complete proteome.
SQ SEQUENCE 319 AA; 35813 MW; 1DB9B1C7CCEA3A9C CRC64;

Query Match
Best Local Similarity 87.9%; Score 29; DB 2; Length 319;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPPLYL 8
DB 70 PRRPYTL 76

RESULT 35
Q87EY1 PRELIMINARY; PRT; 319 AA.
ID Q87EY1
AC Q87EY1;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha.
GN Name=acca; OrderedLocuNames=PD0164;
OS Xylella fastidiosa (strain Temecula / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=183190;
RN [1]
SQ SEQUENCE FROM N.A.
RX MEDLINE=22421331; PubMed=12533478;
RX DOI=10.1128/JB.185.3.1018-1026.2003;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
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RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Teal S.M.,
RA Carier H., Cariero D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.E.,
RA Martins C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Bata G.S., Bianco S.R., Brito M.S., Camnaran F.S., Celestino A.V.,
RA da Cunha A.F., Fenille R.C., Ferro J.A., Pormghieri E.F., Kishi L.T.,
RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sasaki F.T., Seta J.A.D.,
RA de Souza A.A., Trufi D., Tsukumo F., Yanai G.M., Zatos L.G.,
RA Civerolo E.L., Stimpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitajima J.P.;
RT "Comparative analyses of the complete genome sequences of Pierce's
RT disease and citrus variegated chlorosis strains of Xylella
RT fastidiosa.";
RL J. Bacteriol. 185:1018-1026 (2003).
RU EMBL; AE012553; AAO28058.1; -.
DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0006633; P:transferase activity; IEA.
DR GO; GO:0016740; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR01095; Ac-CoA_carboxylA.
DR Pfam; PF03255; ACCA; 1.
DR PRINTS; PR01069; ACCCTFRASEA.
DR TIGRFAMs; TIGR00513; acca; 1.
KM Complete proteome; Transferase.
SQ SEQUENCE 319 AA; 35631 MW; 87B4AEF98620B65C CRC64;

Query Match
Best Local Similarity 87.9%; Score 29; DB 2; Length 319;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPPLYL 8
DB 67 PRRPYTL 73

RESULT 36
Q87MF3 PRELIMINARY; PRT; 319 AA.
ID Q87MF3
AC Q87MF3;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Acetyl-CoA carboxylase, carboxyl transferase alpha subunit.
GN OrderedLocuNames=VP2302;
OS Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
SQ SEQUENCE FROM N.A.
RX STRAIN=RIMD 221063 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Martino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagimoto S.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura K.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749 (2003).
RU EMBL; AP005081; BAC60565.1; -.
DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR01095; Ac-CoA_carboxylA.
DR Pfam; PF03255; ACCA; 1.
DR PRINTS; PR01069; ACCCTFRASEA.
DR TIGRFAMs; TIGR00513; acca; 1.
KM Complete proteome; Transferase.
SQ SEQUENCE 319 AA; 35699 MW; 31F99366BE2A4667 CRC64;
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Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
 Db 70 PRRPYTL 76

RESULT 37

Q8DBE5 PRELIMINARY; PRT; 319 AA.
 AC Q8DBE5; (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Acetyl-CoA carboxylase alpha subunit.
 GN OrderedLocustNames=V11876;
 OS Vibrio vulnificus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
 OC Vibrionaceae; Vibrrio.
 OX NCBI_TaxID=672;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMCP6;
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
 RA Choy H.E.;

RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";
 RL Submitted (DDBJ-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AEO16803; AAO10278.1; -
 DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro: IPR001095; Ac-CoA_carboxylA.

DR Pfam: PF03255; ACCA.1
 DR PRINTS; PRO1069; ACCCTFRPASEA.
 DR TIGRFAMs; TIGR00513; acca; 1.
 KW Complete proteome.
 SQ SEQUENCE 319 AA; 35572 MW; 25D56FDB320DC138 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
 Db 70 PRRPYTL 76

RESULT 38

Q8FLO3 PRELIMINARY; PRT; 319 AA.
 AC Q8FLO3; (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha (EC 6.4.1.2).
 GN Name=acca; OrderedLocustNames=00223;
 OS Escherichia coli O6.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=217992;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=06:1H1 / CFT073 / ATCC 700928;
 RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Rosesch P.,
 RA Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Domeneberg M.S., Blattner F.R.;

RT "Extensive mosaic structure revealed by the complete genome sequence

RT of uropathogenic *Escherichia coli*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 DR EMBL; AEO16755; AAN78715.1; -
 DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro: IPR001095; Ac-CoA_carboxylA.
 DR Pfam; PF03255; ACCA.1.
 DR PRINTS; PRO1069; ACCCTFRPASEA.
 DR TIGRFAMs; TIGR00513; acca; 1.
 KW Complete proteome; Ligase; Transferase.
 SQ SEQUENCE 319 AA; 35287 MW; 1C1F8DE48D8E946 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
 Db 70 PRRPYTL 76

RESULT 39

Q9URV8 PRELIMINARY; PRT; 319 AA.
 AC Q9URV8; (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Acetyl-CoA carboxylase, carboxyl transferase alpha subunit.
 GN OrderedLocustNames=NM81139; NM81177;
 OS *Neisseria meningitidis* (serogroup B).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / Serogroup B;
 RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
 RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
 RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
 RA Dodson R.J., Nelson W.C., Gwinn M.L., Deboy R.T., Peterson J.D.,
 RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
 RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
 RA Clifton H., Clark E.B., Cotton M.D., Uetexback T.R., Knouri H.M.,
 RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizza M.,
 RA Grandi G., Sun L., Smith H.O., Frazer C.M., Moxon E.R., Rappuoli R.,
 RA Venter J.C.;

RT "Complete genome sequence of *Neisseria meningitidis* serogroup B strain MC58.";
 RL Science 287:1809-1815(2000).
 DR EMBL; AEO02465; AAF41562.1; -
 DR EMBL; AEO02462; AAF41527.1; -
 DR PIR; B8119; B8119.
 DR TIGR; NM81139; -
 DR TIGR; NM81177; -
 DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
 DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
 DR InterPro: IPR001095; Ac-CoA_carboxylA.
 DR Pfam; PF03255; ACCA.1.
 DR PRINTS; PRO1069; ACCCTFRPASEA.
 DR TIGRFAMs; TIGR00513; acca; 1.
 KW Complete proteome; Transferase.
 SQ SEQUENCE 319 AA; 35506 MW; CCAE5172FD149D7F CRC64;

Query Match 87.9%; Score 29; DB 2; Length 319;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPPLYL 8
| | | |
Db 67 PQRPYTL 73

RESULT 40

09JUF0 PRELIMINARY; PRT; 319 AA.
ID 09JUF0
AC 09JUF0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative acetyl-CoA carboxylase carboxyl transferase subunit (EC 6.4.1.2).
GN Name=acca; OrderedLocNames=NMA1349;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCB1_TaxID=65699;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=2022255; PubMed=10761919; DOI=10.1038/3500655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagsels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrall B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491."
RT Nature 404:502-506(2000).
RL EMBL: AL162755; CAB84596.1; -
DR PIR; H81903; H81903.
DR GO; GO:0009317; C:acetyl-CoA carboxylase complex; IEA.
DR GO; GO:0003989; F:acetyl-CoA carboxylase activity; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR InterPro; IPR01095; Ac-CoA_carboxylA.
DR Pfam; PF03255; ACCA; 1.
DR PRINTS; PR01069; ACCCTFRASEA.
DR TIGRFAMs; TIGR00513; acca; 1.
KW Complete proteome; Ligase; Transferase.
SQ SEQUENCE 319 AA; 35492 MW; EA753CD5F169BCB0 CRC64;

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 4.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PXPPLYL 8
| | | |
Db 67 PQRPYTL 73

Search completed: March 28, 2005, 08:37:17
Job time : 124 secs

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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:33:43 ; Search time 39 Seconds
(without alignments)
19.737 Million cell updates/sec

Title: US-10-036-918b-4
Perfect score: 33
Sequence: 1 XPRPYXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	90.9	360	2 H97447	probable ferredoxi
2	30	90.9	360	2 A12665	ferredoxin I Atu07
3	30	90.9	1100	2 S43677	protein tyrosine k
4	29	87.9	253	1 C47031	orf1 3'of bah - St
5	29	87.9	312	2 A81389	acetyl-CoA carboxy
6	29	87.9	315	2 I64065	acetyl-CoA carboxy
7	29	87.9	316	2 D83192	acetyl-CoA carboxy
8	29	87.9	319	1 A43452	acetyl-coenzyme A
9	29	87.9	319	2 AB0531	acetyl-coenzyme A
10	29	87.9	319	2 H82836	acetyl-coenzyme A
11	29	87.9	319	2 H81903	probable acetyl-Co
12	29	87.9	319	2 H81119	acetyl-CoA carboxy
13	29	87.9	319	2 C90652	acetyl-CoA carboxy
14	29	87.9	319	2 C85503	acetyl-CoA carboxy
15	29	87.9	319	2 F82100	acetyl-CoA carboxy
16	29	87.9	319	2 AC0130	acetyl-CoA carboxy
17	29	87.9	385	2 A12959	methanesulfonate s
18	29	87.9	385	2 F98323	alkanesulfonate s
19	29	87.9	504	2 A41783	lacthylinin recepto
20	29	87.9	686	2 B75267	prolyl endopeptida
21	29	87.9	1060	2 T31341	ragC protein - Bra
22	29	87.9	1099	2 S48053	protein tyrosine k
23	28	84.8	13	1 UNBO	neurotensin - bovi
24	28	84.8	150	2 D64123	stringent starvati
25	28	84.8	158	2 F82305	stringent starvati
26	28	84.8	165	2 B91141	stringent starvati
27	28	84.8	165	2 JS0666	stringent starvati
28	28	84.8	165	2 H85986	stringent starvati
29	28	84.8	166	2 AD0908	stringent starvati

30	28	84.8	169	2 A28146	neurotensin / neur
31	28	84.8	170	1 UNDG	neurotensin precur
32	28	84.8	171	2 A10432	probable stringent
33	28	84.8	312	2 F87546	transcription regu
34	28	84.8	316	2 F87260	WeeB/TagB/CspF fam
35	28	84.8	389	2 T03612	chalcone synthase
36	28	84.8	389	2 T02970	hypothetical prote
37	28	84.8	390	2 T10742	chalcone synthase
38	28	84.8	514	2 T06585	ammonium transport
39	28	84.8	569	2 S75169	urease (EC 3.5.1.5
40	28	84.8	569	2 C36950	urease (EC 3.5.1.5
41	27	81.8	141	2 T08790	hypothetical prote
42	27	81.8	161	2 H82696	rod shape-determin
43	27	81.8	175	2 T26604	hypothetical prote
44	27	81.8	246	2 T30490	hypothetical prote
45	27	81.8	312	2 F71922	acetyl-coenzyme A
46	27	81.8	312	2 E64589	acetyl-CoA carboxy
47	27	81.8	378	2 AF3320	flavonemoprotein (
48	27	81.8	430	2 T06000	aspartic proteinas
49	27	81.8	430	2 G83710	hypothetical prote
50	27	81.8	556	2 G83710	hypothetical prote
51	27	81.8	569	2 AG2264	urease alpha chain
52	27	81.8	569	2 A97648	urease alpha chain
53	27	81.8	569	2 AG2871	urease alpha subu
54	27	81.8	570	2 S42607	urease (EC 3.5.1.5
55	27	81.8	570	2 AF3458	urease (EC 3.5.1.5
56	27	81.8	622	2 E72754	probable phosphoen
57	27	81.8	790	2 T34293	hypothetical prote
58	27	81.8	790	2 T30249	cell proliferation
59	26	78.8	79	2 B83400	hypothetical prote
60	26	78.8	129	2 S48814	hypothetical prote
61	26	78.8	154	2 S28509	E6 protein - Old w
62	26	78.8	156	2 C56613	virion morphogenes
63	26	78.8	161	2 A12719	conserved hypotet
64	26	78.8	173	2 H82535	ribonuclease Xf261
65	26	78.8	174	2 B71453	hypothetical prote
66	26	78.8	187	2 B97501	hypothetical prote
67	26	78.8	190	2 S48101	xyloglucan endo-1,
68	26	78.8	209	2 A83524	hypothetical prote
69	26	78.8	211	2 T10392	late expression fa
70	26	78.8	212	2 C75636	probable N-acetyl m
71	26	78.8	224	2 T03238	extensin (clone Ex
72	26	78.8	227	2 G70414	conserved hypotet
73	26	78.8	241	2 B49202	cysteine-rich secr
74	26	78.8	253	2 C36808	hypothetical prote
75	26	78.8	256	2 A55652	Oct-binding factor
76	26	78.8	260	2 AB1652	phage related prot
77	26	78.8	260	2 A11587	phage related prot
78	26	78.8	268	2 AC3198	conserved hypotet
79	26	78.8	269	2 E72808	gp69 protein - Myc
80	26	78.8	280	2 T03236	extensin precursor
81	26	78.8	293	2 T48975	xyloglucan endo-tr
82	26	78.8	295	2 S48102	xyloglucan endo-1,
83	26	78.8	300	2 T49748	hypothetical prote
84	26	78.8	306	2 AB3431	hydroxyacylgutath
85	26	78.8	316	2 H81557	conserved hypotet
86	26	78.8	316	2 H85509	ct149 hypothetical
87	26	78.8	316	2 B72113	hypothetical prote
88	26	78.8	318	2 JE0284	Mm-1 cell derived
89	26	78.8	325	2 T33520	hypothetical prote
90	26	78.8	325	2 C95952	hypothetical prote
91	26	78.8	354	2 B81694	UDP-3-O-(R-3-hydro
92	26	78.8	354	2 D71539	probable UDP glucu
93	26	78.8	360	2 F72094	UDP-3-O-(R-3-hydro
94	26	78.8	360	2 F86528	UDP glucosamine N-
95	26	78.8	361	2 B75444	probable phosphino
96	26	78.8	366	1 A24248	inhibin alpha chai
97	26	78.8	390	1 TVTWG	phosphoglycerate k
98	26	78.8	408	2 G83406	conserved hypotet
99	26	78.8	410	2 T06213	probable aspartic
100	26	78.8	410	2 T04372	protein BEA1 - bar

neurotensin / neur
neurotensin precur
probable stringent
transcription regu
WeeB/TagB/CspF fam
chalcone synthase
hypothetical prote
chalcone synthase
ammonium transport
urease (EC 3.5.1.5
urease (EC 3.5.1.5
hypothetical prote
rod shape-determin
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acetyl-coenzyme A
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probable phosphoen
hypothetical prote
cell proliferation
hypothetical prote
hypothetical prote
E6 protein - Old w
virion morphogenes
conserved hypotet
ribonuclease Xf261
hypothetical prote
hypothetical prote
xyloglucan endo-1,
hypothetical prote
late expression fa
probable N-acetyl m
extensin (clone Ex
conserved hypotet
cysteine-rich secr
hypothetical prote
Oct-binding factor
phage related prot
phage related prot
conserved hypotet
gp69 protein - Myc
extensin precursor
xyloglucan endo-tr
xyloglucan endo-1,
hypothetical prote
hydroxyacylgutath
conserved hypotet
ct149 hypothetical
hypothetical prote
Mm-1 cell derived
hypothetical prote
hypothetical prote
UDP-3-O-(R-3-hydro
probable UDP glucu
UDP-3-O-(R-3-hydro
UDP glucosamine N-
probable phosphino
inhibin alpha chai
phosphoglycerate k
conserved hypotet
probable aspartic
protein BEA1 - bar

ALIGNMENTS

RESULT 1

H97447

Probable ferredoxin (P5411) [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
 C/Species: Agrobacterium tumefaciens
 C/Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C/Accession: H97447

R/Gooder, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2322-2328, 2001
 A/Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
 A/Reference number: A97359; PMID:21608551; PMID:11743194
 A/Accession: H97447
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1360 <KUR>

A/Cross-references: UNIPROT:Q8UHF5; GB:AE007869; PIDN:AAK86537.1; PID:g15155697; GSPDB:C
 C/Genetics:
 A:Gene: AGR_C_1321
 A:Map position: circular chromosome
 C/superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferred

Query Match 90.9%; Score 30; DB 2; Length 360;
 Best Local Similarity 71.4%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 77 PRRPYAL 83

RESULT 2

A12665

ferredoxin I Atu0727 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C/Species: Agrobacterium tumefaciens
 C/Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 16-Aug-2004
 C/Accession: A12665

R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
 A/Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A/Reference number: AB2577; PMID:21608550; PMID:11743193
 A/Accession: A12665
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1360 <KUR>

A/Cross-references: UNIPROT:Q8UHF5; GB:AE008688; PIDN:AA4141743.1; PID:g17739094; GSPDB:C
 A/Experimental source: strain C58 (Dupont)
 C/Genetics:
 A:Gene: Atu0727
 A/Map position: circular chromosome
 C/superfamily: Phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferred

Query Match 90.9%; Score 30; DB 2; Length 360;
 Best Local Similarity 71.4%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 77 PRRPYAL 83

RESULT 3

S43677

protein tyrosine kinase JAK3 - rat
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 20-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004
 C/Accession: S43677

R/Takahashi, T.; Shirasawa, T.
 FEBS Lett. 342, 124-128, 1994
 A/Title: Molecular cloning of rat JAK3, a novel member of the JAK family of protein tyros

A/Reference number: S43677; PMID:94192816; PMID:8143863
 A/Accession: S43677
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-1100 <TAK>
 A/Cross-references: UNIPROT:Q63272; GB:D28508; NID:g485811; PIDN:BAA05868.1; PID:d1006416
 C/superfamily: protein kinase homology
 C/Keywords: ATP
 F:515-780/Domain: protein kinase homology <KIN1>
 F:815-1094/Domain: protein kinase homology <KIN2>

Query Match 90.9%; Score 30; DB 2; Length 1100;
 Best Local Similarity 71.4%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 228 PRRPYAL 234

RESULT 4

C47031

orf13 of bah - Streptomyces hygroscopicus
 C/Species: Streptomyces hygroscopicus
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Jul-2004
 C/Accession: C47031

R/Rabaud, A.; Zalcstein, M.; Holt, T.G.; Tizard, R.; Thompson, C.J.
 J. Bacteriol. 173, 4454-4463, 1991
 A/Title: Nucleotide sequence analysis reveals linked N-acetyl hydrolase, thioesterase, tr

A/Reference number: A47031; PMID:91294191; PMID:2066341
 A/Accession: C47031
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-253 <RAI>
 A/Cross-references: UNIPROT:Q03093; GB:M64783; NID:g153172; PIDN:AAA79278.1; PID:g153174
 A/Note: sequence extracted from NCBI backbone (NCBIN:41300, NCBI:P41305)
 C/superfamily: type II thioesterase, NRPS/PKS/S-PAS type; oleoyl-lacetyl-carrier-protein }
 F:16-228/Domain: oleoyl-lacetyl-carrier-protein hydrolase homology <ACPH>

Query Match 87.9%; Score 29; DB 1; Length 253;
 Best Local Similarity 71.4%; Pred. No. 54;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 78 PRRPYAL 84

RESULT 5

A81389

acetyl-CoA carboxylase (EC 6.4.1.2) carboxyltransferase alpha chain Cj0443 [similarity]
 C/Species: Campylobacter jejuni
 C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
 C/Accession: A81389

R/Parthill, J.; Wren, B.W.; Mungall, K.; Kerley, J.M.; Churcher, C.; Basham, D.; Chilling C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; Vanylic, A.; Whitehead, S.; Barrell Nature 403, 665-668, 2000
 A/Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyp
 A/Reference number: A81250; PMID:20150912; PMID:10688204
 A/Accession: A81389
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-312 <PAR>

A/Cross-references: UNIPROT:Q9P162; GB:AL139075; GB:AL111168; NID:g6967817; PIDN:CA874275
 A/Experimental source: serotype O2, strain NCTC 11168
 C/Genetics:
 A:Gene: accA; Cj0443
 C/superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
 C/Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 312;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
| | | | |
Db 60 PRRPYXL 66

RESULT 6

164065
A:Title: CoA carboxylase (EC 6.4.1.2), carboxyltransferase alpha chain - Haemophilus influenzae
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 09-Jul-2004
C/Accession: 164065
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; FINE, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Accession: 164065
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-315 <TTGR>
A:Cross-references: UNIPROT:P43872; GB:U32724; GB:L42023; NID:g1573378; PIND:AAC22065.1;
C/Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
C/Keywords: fatty acid biosynthesis, ligase

Query Match 87.9%; Score 29; DB 2; Length 315;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
| | | | |
Db 66 PRRPYXL 72

RESULT 7

DB3192
A:Title: coenzyme A carboxylase carboxyl transferase (alpha subunit) PA3639 [imported] - F
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: DB3192
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim, J.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: DB3192
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-316 <STO>
A:Cross-references: UNIPROT:Q9HXZ2; GB:AB004783; GB:AB004091; NID:g9949786; PIND:AA60702
C/Genetics:
C/Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain

Query Match 87.9%; Score 29; DB 2; Length 316;
Best Local Similarity 71.4%; Pred. No. 68;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
| | | | |
Db 67 PRRPYXL 73

RESULT 8

A43452

acetyl-CoA carboxylase (EC 6.4.1.2) carboxyltransferase alpha chain [validated] - Escherichia coli
C/Species: Escherichia coli
C/Date: 04-Mar-1993 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004
C/Accession: A43452; D26390; A64743

R/Li, S.-J.; Cronan Jr., J.E.
J. Biol. Chem. 267, 16841-16847, 1992
A:Title: The genes encoding the two carboxyltransferase subunits of Escherichia coli acetyl-CoA carboxylase
A/Reference number: A43452; MUID:92380982; PMID:1355089
A/Accession: A43452
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA; protein

A:Residues: 1-319 <LII>
A:Cross-references: UNIPROT:P30867; GB:M96394; NID:g147321; PIND:AAA70370.1; PID:g147322
A/Note: sequence extracted from NCBI backbone (NCBI:P.111872)
R/Tomasiewicz, H.G.; McHenry, C.S.
J. Bacteriol. 169, 5735-5744, 1987
A:Title: Sequence analysis of the Escherichia coli dnaB gene.
A/Reference number: A91855; MUID:88058791; PMID:3316182
A/Accession: D28390
A:Molecule type: DNA

A:Residues: 1-20 <TON>
A:Cross-references: GB:M19334; GB:M18265; GB:M18266; NID:g450760
R/Baltner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503

A/Accession: A64743
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-319 <BLAT>
A:Cross-references: GB:AB00127; GB:U00096; NID:g1786370; PIND:AAC73296.1; PID:g1786382;
A:Experimental source: strain K-12, substrain MG1655

C/Genetics:
A:Gene: accA
A:Map position: 4.3 min
A:Complex: in E. coli, acetyl-CoA carboxylase is composed of biotin carboxylase (EC 6.3.3.9) and biotin carboxyl carrier protein (BCCP, homodimer) (PIR:BKEC9)

C/Function: <ACC>
A:Description: EC 6.4.1.2 [validated, MUID:7505556]; the acetyl-CoA carboxylase complex
A:Pathway: fatty acid biosynthesis
C/Function: <CTRA>

A:Description: catalyzes the transfer of the carboxyl group from the carboxyl-biotin to
C/Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
C/Keywords: fatty acid biosynthesis, ligase
P.84-119/Region: acyl-CoA binding #status predicted

Query Match 87.9%; Score 29; DB 1; Length 319;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
| | | | |
Db 70 PRRPYXL 76

RESULT 9

AB0531
A:Title: coenzyme A carboxylase carboxyl transferase chain alpha [imported] - Salmonella enterica serovar typhimurium
C/Species: Salmonella enterica subsp. enterica serovar typhimurium
A/Note: this species has also been called Salmonella typhimurium
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C/Accession: AB0531
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, C.; T. Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar typhimurium
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AB0531
A:Status: preliminary
A:Molecule type: DNA

A;Residues: 1-319 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08690.1; PID:G16501513; GSPDB:GN00176
C;Genetics:
A;Gene: STY0255
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPPLYL 8
DB 70 PRRPYTL 76

RESULT 10

H82836
acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha XFO203 [Imported] - Xyl

C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: H82836

R;Annotation: The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: A82515; MUID:20365717; PMID:10910347

A;Note: For a complete list of authors see reference number A59328 below

A;Accession: H82836

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-319 <STM>

A;Cross-references: UNIPROT:Q9PGU5; GB:AE003873; GB:AE003849; NID:G9104992; PIDN:AAF8301

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvares, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carier, H

as-Melo, E.; Docena, C.; El-Dorri, H.; Faciniani, A.P.; Ferreira, A.J.S.

Submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Klieger, J.E.; Kuramae, E.E.; Laig

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J.; de Rosa, V.E.; de Sa, R.G.; Santelli, R.V.; Savasak

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XFO203

C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPPLYL 8
DB 67 PRRPYTL 73

RESULT 11

H81903
probable acetyl-CoA carboxylase (EC 6.4.1.2) carboxyltransferase alpha chain NMA1349 [s

C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: H81903

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel

; Holroyd, S.; Jagels, K.; Leather, S.; Mout, S.; Mungall, K.; Quail, M.A.; Rajandream,

Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: A81775; MUID:20222556; PMID:10761919

A;Accession: H81903

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-319 <PAR>
A;Cross-references: UNIPROT:Q9JUF0; GB:AL162755; GB:AL157959; NID:G7379742; PIDN:CAE84596
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: accA; NMA1349
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPPLYL 8
DB 67 PRRPYTL 73

RESULT 12

B8119
acetyl-CoA carboxylase, carboxyl transferase alpha chain NMB1139, NMB1177 [Imported] - Ne

C;Species: Neisseria meningitidis

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: B8119; G8114

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.

Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;

xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignan, V.; Pizza, M.

Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver

A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.

A;Reference number: A81000; MUID:2015755; PMID:10710307

A;Accession: B8119

A;Molecule type: DNA

A;Residues: 1-319 <DET>

A;Cross-references: UNIPROT:Q9JRV8; GB:AE002462; GB:AE002098; NID:G726363; PIDN:AAF4152;

A;Experimental source: serogroup B, strain MC58

A;Accession: G8114

A;Molecule type: DNA

A;Residues: 1-319 <DET>

A;Cross-references: GB:AE002465; GB:AE002098; NID:G7226401; PIDN:AAF41562.1; PID:G7226414

A;Experimental source: serogroup B, strain MC58

C;Genetics:

A;Gene: NMB1139; NMB1177

C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPPLYL 8
DB 67 PRRPYTL 73

RESULT 13

C90652
acetyl-CoA carboxylase (EC 6.4.1.2) carboxyltransferase alpha chain - Escherichia coli (E

C;Species: Escherichia coli

C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004

C;Accession: C90652

R;Hayashi, T.; Makino, K.; Ohishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.,

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shida, T.; Hattori, M.; Shinagawa, H.

DNA Res. 9, 11-22, 2001

A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom

A;Reference number: A9629; MUID:2156231; PMID:11258796

A;Accession: C90652

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-319 <NAV>

A;Cross-references: UNIPROT:P30867; GB:BA000007; PIDN:BA833610.1; PID:G13359643; GSPDB:GT

A;Experimental source: strain O157:H7, substrain RMD 0509952

C;Genetics:

A;Gene: EC80187

C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain

C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPPLYL 8
DB 70 PXPPLYL 76

RESULT 14

C85503
acetyl-CoA carboxylase (BC 6.4.1.2) carboxyltransferase alpha chain [similarity] - Esche
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: C85503
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
11ler, L.; Grobbeck, E.U.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85503
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <STO>
A;Cross-references: UNIPROT:P30867; GB:AE005174; NID:g12512913; PIDN:AAG54487.1; GSPDB:C
C;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: accA
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPPLYL 8
DB 70 PXPPLYL 76

RESULT 15

F82100
acetyl-CoA carboxylase, carboxyl transferase alpha chain VC2244 [imported] - Vibrio chol
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: F82100
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoti, I.; Sellers, F
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: F82100
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <HRI>
A;Cross-references: UNIPROT:Q9KFW8; GB:AB004296; GB:AE003852; NID:g9656799; PIDN:AAF9538
A;Experimental source: serogroup O1, strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2244
A;Map position: 1
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPPLYL 8
DB 70 PXPPLYL 76

RESULT 16

AC0130
acetyl-CoA carboxylase (BC 6.4.1.2) alpha chain [imported] - Yersinia pestis (strain CO92;
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0130
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; F
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, I
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0130
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-319 <KUR>
A;Cross-references: UNIPROT:Q8ZH52; GB:AL590842; PIDN:CAC69902.1; PID:g15979127; GSPDB:GN
C;Genetics:
A;Gene: accA
C;Superfamily: acetyl-CoA carboxylase, carboxyltransferase alpha chain
C;Keywords: ligase

Query Match 87.9%; Score 29; DB 2; Length 319;
Best Local Similarity 71.4%; Pred. No. 69;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPPLYL 8
DB 70 PXPPLYL 76

RESULT 17

A12959
methanesulfonate sulfonataase Atu3279 [imported] - Agrobacterium tumefaciens (strain C58,
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: A12959
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monke, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McClellan
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I
ster, R.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: A12959
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-385 <KUR>
A;Cross-references: UNIPROT:Q8UAT9; GB:AE008689; PIDN:AL44095.1; PID:g17741662; GSPDB:GN
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu3279
A;Map position: linear chromosome

Query Match 87.9%; Score 29; DB 2; Length 385;
Best Local Similarity 71.4%; Pred. No. 85;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPPLYL 8
DB 171 PXPPLYL 177

RESULT 18

E98323
alkanesulfonate monooxygenase (sulfate starvation-induced protein 6) (spi6) [imported] -
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004
C;Accession: E98323
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent *Agrobacterium tumefaciens*
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: E98323
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-385 <KUR>
 A:Cross-references: UNIPROT:Q8UAT8; GB:AE007870; PIDN:AAK90111.1; PID:915160102; GSPDB:C
 C:Genetics:
 A:Gene: AGR L 3078
 A:Map position: linear chromosome

Query Match 87.9%; Score 29; DB 2; Length 385;
 Best Local Similarity 71.4%; Pred. No. 85;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 171 PRRPYXL 177

RESULT 19

A41783
 tachykinin receptor NKD - fruit fly (*Drosophila melanogaster*)
 C:Species: *Drosophila melanogaster*
 C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Apr-2000
 C:Accession: A41783
 R:Monnier, D.; Colas, J.F.; Roaya, P.; Hen, R.; Borrelli, E.; Maroteaux, L.
 J. Biol. Chem. 267, 1298-1302, 1992
 A:Title: NKD, a developmentally regulated tachykinin receptor in *Drosophila*.
 A:Reference number: A41783; MUID:92112776; PMID:1370464
 A:Accession: A41783
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-504 <MON>
 A:Note: sequence extracted from NCBI backbone (NCBIP:76545)
 C:Genetics:
 A:Gene: FlyBase:TKr86C
 A:Cross-references: FlyBase:FBgn0004841
 C:Superfamily: neurokinin 1 receptor
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 87.9%; Score 29; DB 2; Length 504;
 Best Local Similarity 71.4%; Pred. No. 1.1e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 72 PTRPYXL 78

RESULT 20

B75267
 prolyl endopeptidase - *Deinococcus radiodurans* (strain R1)
 C:Species: *Deinococcus radiodurans*
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
 C:Accession: B75267
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
 M.; Shen, M.; Vamathevan, J.V.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
 S.; Smith, H.O.; Venter, J.C.; Frazer, C.M.
 Science 286, 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: B75267
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-686 <WHI>
 A:Cross-references: UNIPROT:Q9RR17; GB:AE002079; GB:AE000513; NID:G6460315; PIDN:AAF1204
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2503
 A:Map position: 1
 C:Superfamily: prolyl oligopeptidase

Query Match 87.9%; Score 29; DB 2; Length 686;
 Best Local Similarity 71.4%; Pred. No. 1.6e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 396 PRRPYXL 402

RESULT 21

T31341
 tagc protein - *Bradyrhizobium japonicum*
 C:Species: *Bradyrhizobium japonicum*
 C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T31341
 R:Narberhaus, F.; Krümmenacher, P.; Fischer, H.M.; Hennecke, H.
 Mol. Microbiol. 24, 93-104, 1997
 A:Title: Three disparately regulated genes for sigma32-like transcription factors in *Brac*
 A:Reference number: Z21007; MUID:97285751; PMID:9140968
 A:Accession: T31341
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1060 <NAR>
 A:Cross-references: UNIPROT:O69238; EMBL:AJ225023; NID:92961292; PIDN:CAA12353.1; PID:92;
 C:Genetics:
 A:Gene: tagc
 C:Superfamily: cation efflux system membrane protein czca

Query Match 87.9%; Score 29; DB 2; Length 1060;
 Best Local Similarity 71.4%; Pred. No. 2.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 615 PRRPYXL 621

RESULT 22

S48053
 protein tyrosine kinase - mouse
 C:Species: *Mus musculus* (house mouse)
 C>Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 16-Aug-2004
 C:Accession: S48053; S51607
 R:Wlthuhn, B.A.; Silvennoinen, O.; Miura, O.; Lai, K.S.; Cwik, C.; Liu, E.T.; Ihle, J.N
 Nature 370, 153-157, 1994
 A:Title: Involvement of the Jak-3 Janus kinase in signalling by interleukins 2 and 4 in J
 A:Reference number: S48053; MUID:94294024; PMID:8022486
 A:Accession: S48053
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-1099 <WIT>
 A:Cross-references: EMBL:LJ2955
 R:Wlthuhn, B.A.; Silvennoinen, O.; Miura, O.; Lai, K.S.; Cwik, C.; Liu, E.T.; Ihle, J.N
 submitted to the EMBL Data Library, August 1994
 A:Reference number: S51607
 A:Accession: S51607
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-61, A, 63-1099 <WIT>
 A:Cross-references: EMBL:LJ2955; NID:9529239; PIDN:AAA21565.1; PID:9529239
 C:Superfamily: protein kinase homology
 C:Keywords: ATP

F:514-779/Domain: protein kinase homology <KIN1>
 F:815-1093/Domain: protein kinase homology <KIN2>
 F:824-832/Region: protein kinase ATP-binding motif

Query Match 87.9%; Score 29; DB 2; Length 1099;
 Best Local Similarity 71.4%; Pred. No. 2.6e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 1111

Db 228 PGRPYAL 234

RESULT 23

UNBO

neurotensin - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 24-Feb-1995

C:Accession: A01420

R:Caraway, R.; Leeman, S.E.

J. Biol. Chem. 250, 1907-1911, 1975

A:Title: The amino acid sequence of a hypothalamic peptide, neurotensin.

A:Reference number: A92172; MUID:75095678; PMID:1167549

A:Accession: A01420

A:Molecule type: protein

A:Residues: 1-13 <CAR>

A:Experimental source: hypothalamus

R:Caraway, R.; Leeman, S.E.

J. Biol. Chem. 250, 1912-1918, 1975

A:Title: The synthesis of neurotensin.

A:Reference number: A92173; MUID:75095679; PMID:1112838

A:Contents: annotation; synthesis

A:Note: a tripeptide chemically and pharmacologically identical with the natural peptide

C:Superfamily: neurotensin

C:Keywords: neuropeptide; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 84.8%; Score 28; DB 1; Length 13;

Best Local Similarity 71.4%; Pred. No. 3.7;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYL 8

Db 7 PRRPYL 13

RESULT 24

D64123

stringent starvation protein sepb - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 12-Jul-2004

C:Accession: D64123

R:Feilschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kervavag, A.

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodok, A.; Kelley, J.M.; Weidman, J.

; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Furmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: D64123

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-150 <TTGR>

A:Cross-references: UNIPROT:P45206; GB:U32822; GB:I42023; NID:91574265; PIDN:AAC23089.1;

C:Genetics:

A:Gene: sepb

C:Superfamily: ClpX-specific adaptor protein Sspb

Query Match 84.8%; Score 28; DB 2; Length 150;

Best Local Similarity 71.4%; Pred. No. 51;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYL 8

Db 7 PRRPYL 13

RESULT 25

F82305

stringent starvation protein B VC0577 [imported] - Vibrio cholerae (strain N16961 serog

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 12-Jul-2004

C:Accession: F82305

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

Chadson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, P

l.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: F82305

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-158 <HEI>

A:Cross-references: UNIPROT:Q9KUB4; GB:AE004143; GB:AE003852; NID:93655003; PIDN:AAF374E

A:Experimental source: serogroup O1, strain N16961, biotype El Tor

C:Genetics:

A:Gene: VC0577

A:Map position: 1

C:Superfamily: ClpX-specific adaptor protein Sspb

Query Match 84.8%; Score 28; DB 2; Length 158;

Best Local Similarity 71.4%; Pred. No. 54;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYL 8

Db 12 PRRPYL 18

RESULT 26

E91141

stringent starvation protein B [imported] - Escherichia coli (strain O157:H7, substrain f

C:Species: Escherichia coli

C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 12-Jul-2004

C:Accession: E91141

R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.

gasawara, N.; Yasunaga, T.; Kihara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom

A:Reference number: A96629; MUID:21156231; PMID:11258796

A:Accession: E91141

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-165 <HAY>

A:Cross-references: UNIPROT:P25663; GB:BA000007; PIDN:BA837524.1; PID:913363574; GSPDB:GR

A:Experimental source: strain O157:H7, substrain RMD 050952

C:Genetics:

A:Gene: EC84101

C:Superfamily: ClpX-specific adaptor protein Sspb

Query Match 84.8%; Score 28; DB 2; Length 165;

Best Local Similarity 71.4%; Pred. No. 56;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYL 8

Db 8 PRRPYL 14

RESULT 27

JS0666

stringent starvation protein B, sepb - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 12-Jul-2004

C:Accession: JS0666; P65114

R:Williams, M.D.; Ruch, J.A.; Flickinger, M.C.

Gene 109, 21-30, 1991

A:Title: Null mutation in the stringent starvation protein of Escherichia coli disrupts]

A:Reference number: JS0666; MUID:92097948; PMID:1721886

A:Accession: JS0666

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-165 <WLL>

A:Cross-references: UNIPROT:P25663; GB:M69028; NID:9147871; PIDN:AAA24650.1; PID:9147872

R:Battner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997
 A>Title: The complete genome sequence of *Escherichia coli* K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: F65114
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-165 <BLAT>
 A:Cross-references: GB:AE000402; GB:U00096; NID:g1789619; PIDN:AACT6260.1; PID:g1789623;
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: sspB
 C:Superfamily: ClpX-specific adaptor protein SspB

Query Match 84.8%; Score 28; DB 2; Length 165;
 Best Local Similarity 71.4%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 8 PRRPYLL 14

RESULT 28
 H85986
 stringent starvation protein B [imported] - *Escherichia coli* (strain O157:H7, substrain
 C:Species: *Escherichia coli*
 C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 12-Jul-2004
 C:Accession: H85986
 R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; DiMaio, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001
 A>Title: Genome sequence of enterohemorrhagic *Escherichia coli* O157:H7.
 A:Reference number: A85480; MUID:21074935; PMID:11206551
 A:Accession: H85986
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-165 <STO>
 A:Cross-references: UNIPROT:P25663; GB:AE005174; NID:g12517846; PIDN:AA658356.1; GSPDB:C
 A:Experimental source: strain O157:H7, substrain EDL933
 C:Genetics:
 A:Gene: sspB
 C:Superfamily: ClpX-specific adaptor protein SspB

Query Match 84.8%; Score 28; DB 2; Length 165;
 Best Local Similarity 71.4%; Pred. No. 56;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 8 PRRPYLL 14

RESULT 29
 AD0908
 stringent starvation protein B [imported] - *Salmonella enterica* subsp. *enterica* serovar
 C:Species: *Salmonella enterica* subsp. *enterica* serovar Typh
 A:Note: this species has also been called *Salmonella typhi*
 C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 12-Jul-2004
 C:Accession: AD0908
 R:Perkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 Th, T.; Conington, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Mout, S.; O'Garra, P.
 Nature 413, 848-852, 2001
 A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
 A>Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* serov
 A:Reference number: AB0502; MUID:21534947; PMID:11677608
 A:Accession: AD0908
 A:Molecule type: protein
 A:Residues: 1-166 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAD07658.1; PID:g16504405; GSPDB:GN00176
 C:Genetics:
 A:Gene: STY3522

C:Superfamily: ClpX-specific adaptor protein SspB

Query Match 84.8%; Score 28; DB 2; Length 166;
 Best Local Similarity 71.4%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 8 PRRPYLL 14

RESULT 30
 A28146
 neuroligin / neuromedin N precursor - rat
 C:Species: *Rattus norvegicus* (Norway rat)
 C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 09-Jul-2004
 C:Accession: A28146; A56789
 R:Kisilevskis, E.; Bullock, B.; McNeil, S.; Dobner, P.R.
 J. Biol. Chem. 263, 4963-4968, 1988
 A>Title: The rat gene encoding neuroligin and neuromedin N. Structure, tissue-specific e
 A:Reference number: A28146; MUID:88169625; PMID:2832414
 A:Accession: A28146
 A:Molecule type: mRNA
 A:Residues: 1-169 <KIS>
 A:Cross-references: UNIPROT:P20068
 R:Bidard, J.N.; de Nadal, F.; Rovere, C.; Moinier, D.; Laur, J.; Martinez, J.; Cuber, J.C
 Biochem. J. 291, 225-233, 1993
 A>Title: Immunological and biochemical characterization of processing products from the r
 A:Reference number: A56789; MUID:93228610; PMID:8471039
 A:Accession: A56789
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-42 <BID>
 A:Experimental source: medullary thyroid carcinoma 6-23 cell extracts
 A:Note: sequence extracted from NCBI backbone (NCBIP:129397)
 C:Superfamily: neuroligin
 C:Keywords: neuropeptide

Query Match 84.8%; Score 28; DB 2; Length 169;
 Best Local Similarity 71.4%; Pred. No. 58;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 DB 156 PRRPYLL 162

RESULT 31
 UNDC
 neuroligin precursor - dog
 N:Contains: neuromedin N; neuromedin N-125; neuroligin
 C:Species: *Canis lupus familiaris* (dog)
 C>Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C:Accession: A28025; B60319; A60324; J00293; A36372
 R:Dobner, P.R.; Barber, D.J.; Villa-Komaroff, L.; McKernan, C.
 Proc. Natl. Acad. Sci. U.S.A. 84, 3516-3520, 1987
 A>Title: Cloning and sequence analysis of cDNA for the canine neuroligin/neuromedin N pr
 A:Reference number: A28025; MUID:87204168; PMID:3472221
 A:Accession: A28025
 A:Molecule type: mRNA
 A:Residues: 1-170 <DOB>
 A:Cross-references: UNIPROT:P10673; GB:M16443; NID:g164033; PIDN:AAA30878.1; PID:g164034
 R:Mittra, S.P.; Muraki, K.; Brown, D.R.; Parsons, A.M.; Carraway, R.E.
 Regul. Pept. 28, 11-22, 1990
 A>Title: Canine neuroligin, neuroligin(6-13) and neuromedin N. primary structures and
 A:Reference number: A60319; MUID:90222594; PMID:2158127
 A:Accession: B60319
 A:Molecule type: protein
 A:Residues: 143-148 <MIT>
 A:Accession: A60319
 A:Molecule type: protein
 A:Residues: 1-152-163 <MIT>
 R:Mogard, M.H.; Reeve Jr., J.R.; Shively, J.E.; Ben-Avram, C.M.; Eysselein, V.E.; Walsh,

Regul. Pept. 14, 313-321, 1986
A/Title: Isolation and characterization of a neurotensin-like decapeptide from a canine
A/Reference number: A60324; MUID:86314883; PMID:3749527
A/Accession: A60324
A/Molecule type: protein
A/Residues: 154-163 <MOG>
R/Carraway, R.E.; Mitra, S.P.
Biochem. Biophys. Res. Commun. 179, 301-308, 1991
A/Title: Purification of large neuromedin N (NMN) from canine intestine and its identifi
A/Reference number: JN0293; MUID:91354266; PMID:1883355
A/Accession: JN0293
A/Molecule type: protein
A/Residues: 24-43 <CAR>
A/Experimental source: small intestine
R/Carraway, R.E.; Mitra, S.P.
J. Biol. Chem. 265, 8627-8631, 1990
A/Title: Differential processing of neurotensin/neuromedin N precursor(s) in canine brai
A/Reference number: A36272; MUID:90256783; PMID:2341398
A/Accession: A36272
A/Molecule type: protein
A/Residues: 128-147 <CA2>
A/Superfamily: neurotensin
C/Keywords: hormone; neuropeptide; pyroglutamic acid
F/1-23/Domain: signal sequence #status predicted <SIG>
F/24-148/Product: large neuromedin N-125 #status experimental <LNH>
F/143-148/Product: large neuromedin N #status experimental <NMN>
F/151-163/Product: neurotensin #status experimental <NTS>
F/151/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experime

Query Match 84.8%; Score 28; DB 1; Length 170;
Best Local Similarity 71.4%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PRRPYXL 8
Db 157 PRRPYXL 163

RESULT 32
A/0432
Probable stringest starvation protein B sspB [imported] - Yersinia pestis (strain C092)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 12-Jul-2004
C/Accession: A10432
R/Berthill, J.; Wren, B.W.; Thomson, N.R.; Titchell, R.W.; Holden, M.T.G.; Prentice, M.B.
demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett,
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: A10432
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-171 <KUN>
A/Cross-references: UNIPROT:Q8ZB64; GB:AL590842; PIDN:CA92789.1; PID:G15981482; GSPDB:G
A/Genes: sspB
C/Superfamily: ClpX-specific adaptor protein SspB

Query Match 84.8%; Score 28; DB 2; Length 171;
Best Local Similarity 71.4%; Pred. No. 58;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PRRPYXL 8
Db 8 PRRPYXL 14

RESULT 33
F87546
transcription regulator, AraC family [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C/Accession: F87546
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.I.
B.; Lamb, M.T.; Debby, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolome
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: F87546
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-312 <STO>
A/Cross-references: UNIPROT:Q9A5P8; GB:AE005673; NID:G13423936; PIDN:AAK24370.1; GSPDB:G
C/Genetics:
A/Genes: CC2399

Query Match 84.8%; Score 28; DB 2; Length 312;
Best Local Similarity 57.1%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PRRPYXL 8
Db 108 PRRPYXL 114

RESULT 34
F87260
WeeB/TagA/CpsF family protein [imported] - Caulobacter crescentus
C/Species: Caulobacter crescentus
C/Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C/Accession: F87260
R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.I.
B.; Lamb, M.T.; Debby, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolome
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A/Title: Complete Genome Sequence of Caulobacter crescentus.
A/Reference number: A87249; MUID:21173698; PMID:11259647
A/Accession: F87260
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-316 <STO>
A/Cross-references: UNIPROT:Q9ABX5; GB:AE005673; NID:G13421198; PIDN:AAK22082.1; GSPDB:G
C/Genetics:
A/Genes: CC0095

Query Match 84.8%; Score 28; DB 2; Length 316;
Best Local Similarity 71.4%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PRRPYXL 8
Db 28 PRRPYXL 34

RESULT 35
T03612
chalcone synthase homolog - rice
C/Species: Oryza sativa (rice)
C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 15-Mar-2004
C/Accession: T03612
R/Zhang, Y.; Qu, L.; Xie, M.; Gu, H.; Chen, Z.
submitted to the EMBL Data Library, September 1995
A/Description: cDNA sequence of a CHS-like gene from rice flower.
A/Reference number: Z14978
A/Accession: T03612
A/Status: preliminary; translated from GB/EMBL/DDAJ
A/Molecule type: mRNA
A/Residues: 1-389 <ZHA>
A/Cross-references: EMBL:X91811; NID:G1008983; PID:G1008984
A/Experimental source: cv. Zhonghua 10
A/Genes: chsk
C/Superfamily: Type III polyketide synthase

Query Match 84.8%; Score 28; DB 2; Length 389;
 Best Local Similarity 71.4%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPRYL 8
 DB 209 PDRPYDL 215

RESULT 36
 T02970
 hypothetical protein YV2 - rice
 C/Species: Oryza sativa (rice)
 C/Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
 C/Accession: T02970
 R/Hhara, Y.; Hara, C.; Uchimiya, H.
 Plant Mol. Biol. 30, 1181-1193, 1996
 A/Title: Isolation and characterization of two cDNA clones for mRNAs that are abundantly
 A/Reference number: Z14800; MUID:96311007; PMID:8704128
 A/Accession: T02970
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-389 <HH>
 A/Cross-references: UNIPROT:O23811; EMBL:D50576; NID:g2645163; PIDN:BA23618.1; PID:g264
 A/Experimental source: another, cultivar Hayayuki
 C/Superfamily: Type III polyketide synthase

Query Match 84.8%; Score 28; DB 2; Length 389;
 Best Local Similarity 71.4%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPRYL 8
 DB 209 PDRPYDL 215

RESULT 37
 T10742
 chalcone synthase homolog Cns1 - Monterey pine
 C/Species: Pinus radiata (Monterey pine)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Mar-2004
 C/Accession: T10742
 R/Malden, A.R.; Walter, C.; Gardner, R.C.
 submitted to the EMBL Data Library, February 1997
 A/Description: Genes expressed in Pinus radiata male cones.
 A/Reference number: Z17111
 A/Accession: T10742
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-390 <MAL>
 A/Cross-references: EMBL:U90341; NID:g2507616; PID:g2507617
 A/Experimental source: strain 880/607; tissue_type male cone; clone pAM192
 C/Superfamily: Type III polyketide synthase

Query Match 84.8%; Score 28; DB 2; Length 390;
 Best Local Similarity 71.4%; Pred. No. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPRYL 8
 DB 209 PDRPYDL 215

RESULT 38
 T06585
 ammonium transporter 2 - tomato
 C/Species: Lycopersicon esculentum (tomato)
 C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C/Accession: T06585
 R/Lauter, F.R.; Nimmann, O.; Frommer, W.B.
 submitted to the EMBL Data Library, January 1996
 A/Description: Cloning and characterization of the ammonium transporter LeAMT2 from toma
 A/Reference number: Z15776

A/Accession: T06585
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: mRNA
 A/Residues: 1-514 <LAU>
 A/Cross-references: UNIPROT:O04161; EMBL:X95098; PIDN:CAA64475.1
 A/Experimental source: seedling; root hair
 C/Genetics:
 A/Gene: AMT2
 C/Superfamily: ammonium transport protein amt1

Query Match 84.8%; Score 28; DB 2; Length 514;
 Best Local Similarity 71.4%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPRYL 8
 DB 409 PNRPYGL 415

RESULT 39
 S75169
 urease (EC 3.5.1.5) alpha chain - Synechocystis sp. (strain PCC 6803)
 N/Alternate names: protein ell1750
 C/Species: Synechocystis sp.
 A/Variety: PCC 6803
 C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
 C/Accession: S75169
 R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
 DNA Res. 3, 109-136, 1996
 A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
 S.

A/Reference number: S74322; MUID:97061201; PMID:8905231
 A/Accession: S75169
 A/Status: nucleic acid sequence not shown; translation not shown
 A/Molecule type: DNA
 A/Residues: 1-569 <KAN>
 A/Cross-references: UNIPROT:P73061; EMBL:D90903; GB:AE001339; NID:g1652127; PIDN:BA11708;
 A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
 C/Genetics:
 A/Gene: ureC
 C/Superfamily: urease, alpha subunit; urease 62k chain homology
 C/Keywords: hydrolase; metalloprotein; nickel
 F/5-552/Domain: urease 62k chain homology <U62>
 F/136,138,219,362/Binding site: nickel 2 (His, His, Lys, Asp) #status predicted

Query Match 84.8%; Score 28; DB 2; Length 569;
 Best Local Similarity 57.1%; Pred. No. 2.1e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXRPRYL 8
 DB 302 PTRPYTI 308

RESULT 40
 C36950
 urease (EC 3.5.1.5) 61k chain - Bacillus sp. (strain TB-90)
 N/Alternate names: urec protein
 C/Species: Bacillus sp.
 C/Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 16-Aug-2004
 C/Accession: C36950
 R/Maeda, M.; Hidaka, M.; Nakamura, A.; Masaki, H.; Uozumi, T.
 J. Bacteriol. 176, 432-442, 1994
 A/Title: Cloning, sequencing, and expression of thermophilic Bacillus sp. strain TB-90 w
 A/Reference number: A36950; MUID:94117379; PMID:828859
 A/Accession: C36950
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-569 <MAE>
 A/Cross-references: UNIPROT:Q07397; GB:D14439; NID:g393296; PIDN:BA03325.1; PID:g216362
 C/Superfamily: urease, alpha subunit; urease 62k chain homology
 C/Keywords: hydrolase

F;5-552/Domain: urease 62K chain homology <U62>

Query Match 84.8%; Score 28; DB 2; Length 569;
 Best Local Similarity 57.1%; Pred. No. 2.1e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPYPXL 8
 |||||
 :
 Db 302 PTRPYTI 308

Search completed: March 28, 2005, 08:38:06
 Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:33:43 ; Search time 46 Seconds
(without alignments)
57.583 Million cell updates/sec

Title: US-10-036-918B-4
Perfect score: 33
Sequence: 1 XPRPYXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 33100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubppaa/PCr_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppaa/PCrUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	87.9	65	US-10-437-963-110356	Sequence 110356, A
2	29	87.9	78	US-10-424-599-232759	Sequence 232759, A
3	29	87.9	129	US-10-424-599-257546	Sequence 257546, A
4	29	87.9	157	US-10-094-749-2431	Sequence 2431, A
5	29	87.9	216	US-09-863-200-4	Sequence 4, App1
6	29	87.9	216	US-10-407-079-106	Sequence 106, App
7	29	87.9	247	US-10-424-599-201130	Sequence 201130, A
8	29	87.9	281	US-10-282-122A-72786	Sequence 72786, A
9	29	87.9	312	US-10-282-122A-54324	Sequence 54324, A
10	29	87.9	315	US-09-815-242-11014	Sequence 11014, A
11	29	87.9	315	US-10-282-122A-58158	Sequence 58158, A
12	29	87.9	315	US-10-282-122A-67564	Sequence 67564, A
13	29	87.9	316	US-09-815-242-11934	Sequence 11934, A

14	29	87.9	316	US-10-282-122A-66513	Sequence 66513, A
15	29	87.9	317	US-10-282-122A-66958	Sequence 66958, A
16	29	87.9	317	US-10-282-122A-70135	Sequence 70135, A
17	29	87.9	319	US-09-815-242-10048	Sequence 10048, A
18	29	87.9	319	US-09-815-242-13897	Sequence 13897, A
19	29	87.9	319	US-10-282-122A-43192	Sequence 43192, A
20	29	87.9	319	US-10-282-122A-55833	Sequence 55833, A
21	29	87.9	319	US-10-282-122A-59606	Sequence 59606, A
22	29	87.9	319	US-10-282-122A-65080	Sequence 65080, A
23	29	87.9	319	US-10-282-122A-65894	Sequence 65894, A
24	29	87.9	319	US-10-282-122A-68569	Sequence 68569, A
25	29	87.9	319	US-10-282-122A-75293	Sequence 75293, A
26	29	87.9	319	US-10-282-122A-76171	Sequence 76171, A
27	29	87.9	319	US-10-282-122A-77912	Sequence 77912, A
28	29	87.9	319	US-10-282-122A-77971	Sequence 77971, A
29	29	87.9	320	US-10-282-122A-68469	Sequence 68469, A
30	29	87.9	321	US-10-282-122A-51090	Sequence 51090, A
31	29	87.9	323	US-10-282-122A-47697	Sequence 47697, A
32	29	87.9	323	US-10-282-122A-50581	Sequence 50581, A
33	29	87.9	331	US-10-424-599-215226	Sequence 215226, A
34	29	87.9	392	US-10-437-963-145135	Sequence 145135, A
35	29	87.9	432	US-10-278-141-4	Sequence 4, App1
36	29	87.9	432	US-10-296-081-4	Sequence 4, App1
37	29	87.9	450	US-10-400-991-20	Sequence 20, App1
38	29	87.9	455	US-10-156-761-13950	Sequence 13950, A
39	29	87.9	569	US-10-425-114-70896	Sequence 70896, A
40	29	87.9	747	US-10-425-114-51374	Sequence 51374, A
41	29	87.9	1061	US-10-437-963-184903	Sequence 184903, A
42	29	87.9	1099	US-09-397-967-16	Sequence 16, App1
43	29	87.9	8	US-09-863-971A-8	Sequence 8, App1
44	29	84.8	8	US-09-864-011A-8	Sequence 8, App1
45	28	84.8	8	US-09-981-206A-8	Sequence 8, App1
46	28	84.8	8	US-09-981-271A-8	Sequence 8, App1
47	28	84.8	8	US-09-757-332A-8	Sequence 8, App1
48	28	84.8	8	US-09-757-333D-8	Sequence 8, App1
49	28	84.8	8	US-09-978-725A-8	Sequence 8, App1
50	28	84.8	8	US-09-071-779-8	Sequence 8, App1
51	28	84.8	8	US-10-654-033-8	Sequence 8, App1
52	28	84.8	8	US-10-847-257-8	Sequence 8, App1
53	28	84.8	13	US-09-985-672-2	Sequence 2, App1
54	28	84.8	13	US-09-988-792-4	Sequence 4, App1
55	28	84.8	13	US-09-988-792-14	Sequence 14, App1
56	28	84.8	13	US-10-050-200-21	Sequence 21, App1
57	28	84.8	13	US-10-265-099-1	Sequence 1, App1
58	28	84.8	13	US-10-198-697-1	Sequence 1, App1
59	28	84.8	13	US-10-695-516-8	Sequence 8, App1
60	28	84.8	13	US-10-167-627-66	Sequence 66, App1
61	28	84.8	13	US-10-739-111A-1	Sequence 1, App1
62	28	84.8	13	US-10-839-017-4	Sequence 4, App1
63	28	84.8	51	US-10-437-963-132088	Sequence 132088, A
64	28	84.8	66	US-10-424-599-169926	Sequence 169926, A
65	28	84.8	101	US-10-437-963-176654	Sequence 176654, A
66	28	84.8	148	US-10-767-701-51773	Sequence 51773, A
67	28	84.8	165	US-09-741-669-350	Sequence 350, App
68	28	84.8	169	US-09-927-565A-3	Sequence 3, App1
69	28	84.8	169	US-09-927-565A-4	Sequence 4, App1
70	28	84.8	170	US-09-927-565A-1	Sequence 1, App1
71	28	84.8	170	US-10-241-220-111	Sequence 111, App
72	28	84.8	170	US-10-295-027-316	Sequence 316, App
73	28	84.8	180	US-10-437-963-202235	Sequence 202235, A
74	28	84.8	308	US-10-437-963-115140	Sequence 115140, A
75	28	84.8	360	US-09-829-378-6	Sequence 6, App1
76	28	84.8	360	US-09-829-378-5	Sequence 5, App1
77	28	84.8	389	US-10-337-963-103658	Sequence 7, App1
78	28	84.8	412	US-09-829-378-2	Sequence 2, App1
79	28	84.8	414	US-10-437-963-165801	Sequence 165801, A
80	28	84.8	429	US-10-437-963-200465	Sequence 200465, A
81	28	84.8	444	US-10-156-761-11122	Sequence 11122, A
82	28	84.8	470	US-10-194-527-6	Sequence 6, App1
83	28	84.8	476	US-10-437-963-166866	Sequence 166866, A
84	28	84.8	479	US-10-205-823-210	Sequence 210, App
85	28	84.8	497	US-10-437-963-136383	Sequence 136383, A
86	28	84.8	499	US-10-437-963-148518	Sequence 148518, A

87 28 84.8 566 15 US-10-282-122A-44964 Sequence 44964, A
88 28 84.8 568 15 US-10-282-122A-47638 Sequence 47638, A
89 28 84.8 568 15 US-10-282-122A-50238 Sequence 50238, A
90 28 84.8 649 16 US-10-437-963-153365 Sequence 153365,
91 28 84.8 786 13 US-10-002-344A-221 Sequence 221, App
92 28 84.8 786 17 US-10-958-862-221 Sequence 221, App
93 28 84.8 896 14 US-10-174-677-36 Sequence 36, Appl
94 28 84.8 896 15 US-10-367-978-14 Sequence 14, Appl
95 28 84.8 1030 10 US-09-894-159-72 Sequence 72, Appl
96 28 84.8 1040 15 US-10-211-462-157 Sequence 157, Appl
97 28 84.8 1093 10 US-09-894-159-71 Sequence 71, Appl
98 28 84.8 1279 14 US-10-251-385-293 Sequence 293, App
99 28 84.8 2142 16 US-10-437-963-180052 Sequence 180052,
100 27 81.8 71 15 US-10-424-599-270245 Sequence 270245,

ALIGNMENTS

RESULT 1

US-10-437-963-110356
; Sequence 110356, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437, 963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 110356.
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_14427C.1.pep
US-10-437-963-110356

Query Match 87.9%; Score 29; DB 16; Length 65;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8

DB 51 PRRPYL 57

RESULT 2

US-10-424-599-232759
; Sequence 232759, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 232759
; LENGTH: 78
; TYPE: PRT

; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1) ..(78)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52205C.1.pep
US-10-424-599-232759

Query Match 87.9%; Score 29; DB 15; Length 78;
Best Local Similarity 71.4%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
DB 40 PRRPYSL 46

RESULT 3

US-10-424-599-257546
; Sequence 257546, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424, 599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 257546
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_74589C.1.pep
US-10-424-599-257546

Query Match 87.9%; Score 29; DB 15; Length 129;
Best Local Similarity 71.4%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8

DB 34 PRRPYDL 40

RESULT 4

US-10-094-749-2431
; Sequence 2431, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKA, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOTYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO


```

; TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2431
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2431

Query Match      87.9%; Score 29; DB 15; Length 157;
Best Local Similarity 71.4%; Pred. No. 3.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PRRPYXL 8
Db      43 PRRPYXL 49

RESULT 5
US-09-863-200-4
; Sequence 4, Application US/09863200
; Publication No. US20020039762A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Gluckemann, Maria
; TITLE OF INVENTION: 26908 NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 38155-20014.00
; CURRENT APPLICATION NUMBER: US/09/863,200
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/206,019
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus amino acid
US-09-863-200-4

Query Match      87.9%; Score 29; DB 9; Length 216;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PRRPYXL 8
Db      191 PRRPYXL 197

RESULT 6
US-10-407-079-106
; Sequence 106, Application US/10407079
; Publication No. US20030215860A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Gluckemann, Maria A.
; APPLICANT: Siles-Santiago, Inmaculada
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Galvin, Katherine M.
; TITLE OF INVENTION: 18636, 2466, 43238, 1983, 52881, 2398,
; TITLE OF INVENTION: 45449, 50289, 52872 AND 26908 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MP103-0510MIM
; CURRENT APPLICATION NUMBER: US/10/407,079
; CURRENT FILING DATE: 2003-04-03
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; PRIOR APPLICATION NUMBER: US 10/226,102
; PRIOR FILING DATE: 2002-08-22
; PRIOR APPLICATION NUMBER: US 60/314,041
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 10/225,094
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,185
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: US 10/272,417
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 09/715,790
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/191,845
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: US 10/282,837
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US 09/796,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; PRIOR FILING DATE: 2000-02-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Amino acid consensus sequence
US-10-407-079-106

Query Match      87.9%; Score 29; DB 15; Length 216;
Best Local Similarity 71.4%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PRRPYXL 8
Db      191 PRRPYXL 197

RESULT 7
US-10-424-599-201130
; Sequence 201130, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovacic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 201130
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(247)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_23646C.1.pep
US-10-424-599-201130

Query Match      87.9%; Score 29; DB 15; Length 247;
Best Local Similarity 71.4%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PRRPYXL 8
Db      191 PRRPYXL 197
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Db 80 PRRPYL 86

RESULT 8

US-10-282-122A-72786

; Sequence 72786, Application US/10282122A
; Publication No. US20040029129A1

GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; PRIORITY FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

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; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; Publication No. US20040029129A1

GENERAL INFORMATION:

; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A

; PRIORITY FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078

; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848

; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727

; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335

; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347

; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578

; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931

; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636

; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

; PRIOR FILING DATE: 2001-02-16

; PRIOR APPLICATION NUMBER: 60/269,308

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; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11014
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
; US-09-815-242-11014

Query Match      87.9%; Score 29; DB 9; Length 315;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PRRPYXL 8
DB      66 PRRPYTL 72

RESULT 11
US-10-282-122A-58158
; Sequence 58158, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67564
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Pseudomonas putida
; US-10-282-122A-67564

Query Match      87.9%; Score 29; DB 15; Length 315;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58158
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
; US-10-282-122A-58158

Query Match      87.9%; Score 29; DB 15; Length 315;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PRRPYXL 8
DB      66 PRRPYTL 72

RESULT 12
US-10-282-122A-67564
; Sequence 67564, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67564
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Pseudomonas putida
; US-10-282-122A-67564

Query Match      87.9%; Score 29; DB 15; Length 315;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Db 67 PRRPYTL 73

RESULT 13

US-09-815-242-11934
Sequence 11934, Application US/09815242
Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.

APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: Prokaryotes

FILE REFERENCE: ELITRA.011A

CURRENT APPLICATION NUMBER: US/09/815,242

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11934

LENGTH: 316

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-09-815-242-11934

Query Match 87.9%; Score 29; DB 9; Length 316;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYTL 8

Db 67 PRRPYTL 73

RESULT 14

US-10-282-122A-66513

Sequence 66513, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 66513

LENGTH: 316

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

US-10-282-122A-66513

Query Match 87.9%; Score 29; DB 15; Length 316;
Best Local Similarity 71.4%; Pred. No. 6.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYTL 8

Db 67 PRRPYTL 73

RESULT 15

US-10-282-122A-66958

Sequence 66958, Application US/10282122A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.

APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A

PRIOR FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

```

; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 66958
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Pasteurella multocida
; US-10-282-122A-66958

Query Match      87.9%; Score 29; DB 15; Length 317;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PRRPYTL 8
DB      68 PRRPYTL 74

RESULT 16
; US-10-282-122A-70135
; Sequence 70135, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Foreysch, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: Patent version 3.1
; SEQ ID NO 70135
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Pseudomonas syringae
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```

US-10-282-122A-70135
Query Match      87.9%; Score 29; DB 15; Length 317;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PRRPYTL 8
DB      69 PRRPYTL 75

RESULT 17
; US-09-815-242-10048
; Sequence 10048, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10048
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Escherichia coli
; US-09-815-242-10048

Query Match      87.9%; Score 29; DB 9; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PRRPYTL 8
DB      70 PRRPYTL 76

RESULT 18
; US-09-815-242-13897
; Sequence 13897, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
```

;; TITLE OF INVENTION: Identification of Essential Genes in
;; FILE REFERENCE: ELITRA.011a
;; CURRENT APPLICATION NUMBER: US/09/815,242
;; PRIOR FILING DATE: 2001-03-21, 078
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; NUMBER OF SEQ ID NOS: 14110
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13897
;; LENGTH: 319
;; TYPE: PRT
;; ORGANISM: Salmonella typhi
US-09-815-242-13897

Query Match 87.9%; Score 29; DB 9; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKRPPYL 8
DB 70 PQRPPYL 76

RESULT 19
US-10-282-122A-43192
;; Sequence 43192; Application US/10282122A
;; Publication No. US20040029129A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Liangsu
;; APPLICANT: Zamudio, Carlos
;; APPLICANT: Malone, Cheryl
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Karl
;; APPLICANT: Zyskind, Judith
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John
;; APPLICANT: Carr, Grant
;; APPLICANT: Yamamoto, Robert
;; APPLICANT: Forsyth, R.
;; APPLICANT: Xu, H.
;; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;; FILE REFERENCE: ELITRA.034A
;; CURRENT APPLICATION NUMBER: US/10/282,122A
;; CURRENT FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22

;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 43192
;; LENGTH: 319
;; TYPE: PRT
;; ORGANISM: Escherichia coli
US-10-282-122A-43192

Query Match 87.9%; Score 29; DB 15; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PKRPPYL 8
DB 70 PQRPPYL 76

RESULT 20
US-10-282-122A-55833
;; Sequence 55833; Application US/10282122A
;; Publication No. US20040029129A1
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Liangsu
;; APPLICANT: Zamudio, Carlos
;; APPLICANT: Malone, Cheryl
;; APPLICANT: Haselbeck, Robert
;; APPLICANT: Ohlsen, Karl
;; APPLICANT: Zyskind, Judith
;; APPLICANT: Wall, Daniel
;; APPLICANT: Trawick, John
;; APPLICANT: Carr, Grant
;; APPLICANT: Yamamoto, Robert
;; APPLICANT: Forsyth, R.
;; APPLICANT: Xu, H.
;; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
;; FILE REFERENCE: ELITRA.034A
;; CURRENT APPLICATION NUMBER: US/10/282,122A
;; CURRENT FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 55833
;; LENGTH: 319
;; TYPE: PRT
;; ORGANISM: Enterobacter cloacae
US-10-282-122A-55833

Query Match 87.9%; Score 29; DB 15; Length 319;

Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
DB 70 PRRPYTL 76

RESULT 21

US-10-282-122A-59606
; Sequence 59606, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59606
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-10-282-122A-59606

Query Match 87.9%; Score 29; DB 15; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
DB 70 PRRPYTL 76

RESULT 22

US-10-282-122A-65080
; Sequence 65080, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu

; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A

; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20

; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21

; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23

; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26

; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06

; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09

; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23

; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22

; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09

; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16

; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65080
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-282-122A-65080

Query Match 87.9%; Score 29; DB 15; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
DB 67 PRRPYTL 73

RESULT 23

US-10-282-122A-65894
; Sequence 65894, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A

```

; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 65894
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-10-282-122A-65894

```

```

Query Match      87.9%; Score 29; DB 15; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 PRRPYL 8
DB      67 PRRPYL 73

```

```

RESULT 24
US-10-282-122A-68569
; Sequence 68569, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625

```

```

; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 68569
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-10-282-122A-68569

```

```

Query Match      87.9%; Score 29; DB 15; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

QY      2 PRRPYL 8
DB      70 PRRPYL 76

```

```

RESULT 25
US-10-282-122A-75293
; Sequence 75293, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 75293
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Salmonella typhimurium

```


US-10-282-122A-75293

Query Match 87.9%; Score 29; DB 15; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PRRPYXL 8
Db 70 PRRPYTL 76

RESULT 26

US-10-282-122A-76171
; Sequence 76171, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76171
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Salmonella typhi
US-10-282-122A-76171

Query Match 87.9%; Score 29; DB 15; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PRRPYXL 8
Db 70 PRRPYTL 76

RESULT 27
US-10-282-122A-77412
; Sequence 77412, Application US/10282122A

Publication No. US20040029129A1

; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77412
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-10-282-122A-77412

Query Match 87.9%; Score 29; DB 15; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PRRPYXL 8
Db 70 PRRPYTL 76

RESULT 28
US-10-282-122A-77971
; Sequence 77971, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

```

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 77971
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Versinia pectis
; US-10-282-122A-77971

Query Match      87.9%; Score 29; DB 15; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PKRPPYL 8
Db      70 PRRPYTL 76

RESULT 29
; US-10-282-122A-68469
; Sequence 68469, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
```

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; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68469
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Proteus mirabilis
; US-10-282-122A-68469

Query Match      87.9%; Score 29; DB 15; Length 320;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 PKRPPYL 8
Db      71 PRRPYTL 77

RESULT 30
; US-10-282-122A-51090
; Sequence 51090, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51090
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LENGTH: 321
TYPE: PRT
ORGANISM: Bordetella pertussis
US-10-282-122A-51090

Query Match 87.9%; Score 29; DB 15; Length 321;
Best Local Similarity 71.4%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXPPLYL 8
DB 67 PXPPLYL 73

RESULT 31
US-10-282-122A-47697
Sequence 47697, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyckind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: EITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 47697
LENGTH: 323
TYPE: PRT
ORGANISM: Burkholderia cepacia
US-10-282-122A-47697

Query Match 87.9%; Score 29; DB 15; Length 323;
Best Local Similarity 71.4%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXPPLYL 8
DB 67 PXPPLYL 73

RESULT 32
US-10-282-122A-50581
Sequence 50581, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyckind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: EITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50581
LENGTH: 323
TYPE: PRT
ORGANISM: Burkholderia mallei
US-10-282-122A-50581

Query Match 87.9%; Score 29; DB 15; Length 323;
Best Local Similarity 71.4%; Pred. No. 6.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXPPLYL 8
DB 67 PXPPLYL 73

RESULT 33
US-10-424-599-215226
Sequence 215226, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J
APPLICANT: Kovacic, David K
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 215226
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_36374C.1.pep
US-10-424-599-215226

Query Match 87.9%; Score 29; DB 15; Length 331;
Best Local Similarity 71.4%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
DB 293 PRRPYXL 299

RESULT 34
US-10-437-963-145135
; Sequence 145135, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbaux, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 145135
; LENGTH: 392
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_45883C.1.pep
US-10-437-963-145135

Query Match 87.9%; Score 29; DB 16; Length 392;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
DB 364 PRRPYXL 370

RESULT 35
US-10-278-141-4
; Sequence 4, Application US/10278141
; Publication No. US20030138818A1
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Dzung Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOUTLEY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Nardinder K.
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: YUE, Henry
; APPLICANT: HAFALIA, April
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti

; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0096 USA
; CURRENT APPLICATION NUMBER: US/10/278,141
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 60/208,834
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/207,566
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US01/16285
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/205,628
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 60/208,861
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/206,222
; PRIOR FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 4
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030138818A1 1258785CD1
US-10-278-141-4

Query Match 87.9%; Score 29; DB 14; Length 432;
Best Local Similarity 71.4%; Pred. No. 8.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
DB 393 PRRPYXL 399

RESULT 36
US-10-296-081-4
; Sequence 4, Application US/10296081
; Publication No. US20030220477A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: PATTERSON, Chandra
; APPLICANT: LU, Dzung Aina M.
; APPLICANT: THORNTON, Michael
; APPLICANT: LU, Yan
; APPLICANT: TRIBOUTLEY, Catherine M.
; APPLICANT: GRAUL, Richard
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: WALIA, Nardinder K.
; APPLICANT: NGUYEN, Daniel B.
; APPLICANT: YUE, Henry
; APPLICANT: HAFALIA, April
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LAL, Preeti
; APPLICANT: REDDY, Roopa
; APPLICANT: KALLICK, Deborah A.
; APPLICANT: TANG, Y. Tom
; APPLICANT: AU-YOUNG, Janice
; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
; FILE REFERENCE: PI-0096 PCT
; CURRENT APPLICATION NUMBER: US/10/296,081
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/205,628; 60/206,222; 60/207,566; 60/208,834; 60/208,861
; PRIOR FILING DATE: 2000-05-18; 2000-05-22; 2000-05-25; 2000-06-02; 2000-06-02
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 4

LENGTH: 432
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: incyte ID No. US20030220477A1 1258785CD1
US-10-296-081-4

Query Match 87.9%; Score 29; DB 15; Length 432;
Best Local Similarity 71.4%; Pred. No. 8.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
Db 393 PDRPYSL 399

RESULT 37
US-10-400-991-20
Sequence 20, Application US/10400991
Publication No. US20030224417A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Glucksmann, Maria A.
APPLICANT: Weich, Nadine S.
APPLICANT: Hunter, John J.
APPLICANT: White, David
APPLICANT: Macbeth, Kyle J.
APPLICANT: Williamson, Mark J.
APPLICANT: Meyers, Rachel E.
TITLE OF INVENTION: 14400, 2838, 14618, 15334, 14274, 32164,
TITLE OF INVENTION: 39404, 38911, 26904, 31237, 18057, 16405, 23224,
TITLE OF INVENTION: 27423, 32700, 32712 AND 12216, NOVEL SEVEN-TRANSMEMBRANE
TITLE OF INVENTION: PROTEINS/G-PROTEIN COUPLES RECEPTORS
FILE REFERENCE: MP103-0240NMIM
CURRENT APPLICATION NUMBER: US/10/400, 991
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: US 10/190, 469
PRIOR FILING DATE: 2002-07-05
PRIOR APPLICATION NUMBER: US 09/439, 159
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/137, 063
PRIOR FILING DATE: 1998-08-20
PRIOR APPLICATION NUMBER: US 10/167, 192
PRIOR FILING DATE: 2002-06-11
PRIOR APPLICATION NUMBER: US 09/420, 187
PRIOR FILING DATE: 1999-10-18
PRIOR APPLICATION NUMBER: US 09/173, 869
PRIOR FILING DATE: 1998-10-16
PRIOR APPLICATION NUMBER: US 10/339, 056
PRIOR FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: US 09/377, 429
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US 09/136, 726
PRIOR FILING DATE: 1998-08-19
PRIOR APPLICATION NUMBER: US 09/911, 583
PRIOR FILING DATE: 2001-07-24
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 450
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-400-991-20

Query Match 87.9%; Score 29; DB 15; Length 450;
Best Local Similarity 71.4%; Pred. No. 8.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PRRPYXL 8
Db 157 PSRPYVL 163

Db 411 PDRPYSL 417

RESULT 38
US-10-156-761-13950
Sequence 13950, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156, 761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13950
LENGTH: 455
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-13950

Query Match 87.9%; Score 29; DB 14; Length 455;
Best Local Similarity 71.4%; Pred. No. 9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
Db 347 PLRPYAL 353

RESULT 39
US-10-425-114-70896
Sequence 70896, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5313)B
CURRENT APPLICATION NUMBER: US/10/425, 114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 70896
LENGTH: 569
TYPE: PRT
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: LIB3150-018-B2_FLI.pep
US-10-425-114-70896

Query Match 87.9%; Score 29; DB 15; Length 569;
Best Local Similarity 71.4%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PRRPYXL 8
Db 157 PSRPYVL 163

RESULT 40

US-10-425-114-51274

; Sequence 51274, Application US/10425114

; Publication No. US20040034888A1

; GENERAL INFORMATION:

; APPLICANT: Liu, Jindong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovacic, David K.

; APPLICANT: Screen, Steven E

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

; FILE REFERENCE: 38-21 (5313) B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ. ID NOS: 73128

; SEQ. ID NO 51274

; LENGTH: 747

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3150-094-A6_Flt.pap

US-10-425-114-51274

Query Match 87.9%; Score 29; DB 15; Length 747;

Best Local Similarity 71.4%; Pred. No. 1.5e+03;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8

DB 154 PSRRPYLL 160

Search completed: March 28, 2005, 08:39:57
Job time : 47 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:33:43 ; Search time 44 Seconds
(without alignments)
13.573 Million cell updates/sec

Title: US-10-036-918B-4
Perfect score: 33
Sequence: 1 XPRPYXL 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Issued_Patents_AA:*
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3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	90.9	1100	1 US-08-357-598-11	Sequence 11, Appl
2	30	90.9	1100	2 US-09-003-289-11	Sequence 11, Appl
3	30	90.9	1100	5 PCT-US95-16435-11	Sequence 11, Appl
4	29	87.9	323	4 US-09-543-681A-6625	Sequence 6625, Ap
5	29	87.9	323	4 US-09-489-039A-12281	Sequence 12281, A
6	29	87.9	328	4 US-09-543-681A-4495	Sequence 4495, Ap
7	29	87.9	332	4 US-09-252-991A-21222	Sequence 21222, A
8	29	87.9	1098	3 US-08-946-994-17	Sequence 17, Appl
9	29	87.9	1099	3 US-08-665-574C-16	Sequence 16, Appl
10	29	87.9	1912	4 US-09-949-016-10490	Sequence 10490, A
11	28	84.8	7	4 US-09-528-200-179	Sequence 179, App
12	28	84.8	8	3 US-09-484-318-7	Sequence 7, Appl
13	28	84.8	8	3 US-09-484-319-7	Sequence 7, Appl
14	28	84.8	8	3 US-09-484-320-7	Sequence 7, Appl
15	28	84.8	8	3 US-09-484-321-7	Sequence 7, Appl
16	28	84.8	8	3 US-09-484-323-7	Sequence 7, Appl
17	28	84.8	8	3 US-09-325-769-8	Sequence 8, Appl
18	28	84.8	8	3 US-09-636-170-7	Sequence 7, Appl
19	28	84.8	8	3 US-09-637-518-7	Sequence 7, Appl
20	28	84.8	8	4 US-09-528-200-178	Sequence 178, App
21	28	84.8	8	4 US-09-863-971A-8	Sequence 8, Appl
22	28	84.8	8	4 US-09-864-011A-8	Sequence 8, Appl
23	28	84.8	8	4 US-09-978-725A-8	Sequence 8, Appl
24	28	84.8	9	4 US-09-528-200-177	Sequence 177, App
25	28	84.8	10	4 US-09-528-200-194	Sequence 194, App
26	28	84.8	12	1 US-08-141-324-6	Sequence 6, Appl
27	28	84.8	12	1 US-08-541-902-6	Sequence 6, Appl

28	28	84.8	12	3 US-09-202-832-4	Sequence 4, Appl
29	28	84.8	13	1 US-07-714-540-8	Sequence 8, Appl
30	28	84.8	13	1 US-08-428-468-11	Sequence 11, Appl
31	28	84.8	13	2 US-08-747-137-117	Sequence 117, App
32	28	84.8	13	2 US-08-737-299A-1	Sequence 1, Appl
33	28	84.8	13	3 US-09-334-254A-1	Sequence 1, Appl
34	28	84.8	13	3 US-09-289-693-1	Sequence 2, Appl
35	28	84.8	13	3 US-09-355-869-2	Sequence 8, Appl
36	28	84.8	13	3 US-09-605-990-8	Sequence 8, Appl
37	28	84.8	13	3 US-09-420-797B-8	Sequence 8, Appl
38	28	84.8	13	3 US-09-605-991-8	Sequence 8, Appl
39	28	84.8	13	4 US-09-609-534-8	Sequence 8, Appl
40	28	84.8	13	4 US-09-528-200-10	Sequence 10, Appl
41	28	84.8	13	4 US-09-528-200-161	Sequence 161, App
42	28	84.8	13	4 US-09-528-200-162	Sequence 162, App
43	28	84.8	13	4 US-09-606-247-8	Sequence 8, Appl
44	28	84.8	13	4 US-10-265-099-1	Sequence 1, Appl
45	28	84.8	14	1 US-08-255-272-4	Sequence 4, Appl
46	28	84.8	134	5 PCT-US93-07213-15	Sequence 15, Appl
47	28	84.8	165	4 US-09-489-039A-13714	Sequence 13714, A
48	28	84.8	169	3 US-09-002-114-3	Sequence 3, Appl
49	28	84.8	169	3 US-09-002-114-4	Sequence 4, Appl
50	28	84.8	170	3 US-09-002-114-1	Sequence 1, Appl
51	28	84.8	171	4 US-09-949-016-7377	Sequence 7377, Ap
52	28	84.8	186	4 US-09-248-796A-16073	Sequence 16073, A
53	28	84.8	231	4 US-09-902-540-10807	Sequence 10807, A
54	28	84.8	240	4 US-09-902-540-16005	Sequence 16005, A
55	28	84.8	281	4 US-09-248-796A-16074	Sequence 16074, A
56	28	84.8	317	4 US-09-252-991A-29303	Sequence 29303, A
57	28	84.8	322	4 US-09-902-540-15237	Sequence 15237, A
58	28	84.8	567	4 US-09-328-352-5912	Sequence 5912, Ap
59	28	84.8	568	1 US-07-732-242C-3	Sequence 3, Appl
60	28	84.8	1279	4 US-09-170-496D-293	Sequence 293, App
61	28	84.8	1279	4 US-09-364-425B-58	Sequence 58, Appl
62	27	81.8	169	4 US-09-270-767-75831	Sequence 75831, A
63	27	81.8	169	4 US-09-270-767-53048	Sequence 53048, A
64	27	81.8	551	4 US-09-489-039A-9510	Sequence 9510, Ap
65	27	81.8	726	3 US-09-129-075-4	Sequence 4, Appl
66	27	81.8	726	3 US-09-346-237-3	Sequence 3, Appl
67	27	81.8	726	3 US-09-346-237-13	Sequence 13, Appl
68	27	81.8	726	3 US-09-544-123-4	Sequence 4, Appl
69	27	81.8	915	3 US-09-346-237-2	Sequence 2, Appl
70	26	78.8	20	3 US-08-602-999A-314	Sequence 314, App
71	26	78.8	20	4 US-09-500-124-314	Sequence 314, App
72	26	78.8	46	3 US-08-640-737-43	Sequence 43, Appl
73	26	78.8	100	4 US-09-252-991A-32041	Sequence 32041, A
74	26	78.8	100	1 US-08-482-577B-27	Sequence 27, Appl
75	26	78.8	105	3 US-08-478-097A-22	Sequence 22, Appl
76	26	78.8	105	3 US-08-289-222B-31	Sequence 31, Appl
77	26	78.8	105	3 US-09-218-176-10	Sequence 10, Appl
78	26	78.8	105	3 US-09-054-568B-31	Sequence 31, Appl
79	26	78.8	105	3 US-08-931-858B-169	Sequence 169, App
80	26	78.8	105	3 US-08-961-739-169	Sequence 169, App
81	26	78.8	105	4 US-09-128-026-169	Sequence 22, Appl
82	26	78.8	105	4 US-09-496-398-22	Sequence 22, Appl
83	26	78.8	105	4 US-09-220-616-169	Sequence 169, App
84	26	78.8	105	4 US-09-374-988C-61	Sequence 61, Appl
85	26	78.8	105	4 US-09-220-577-169	Sequence 169, App
86	26	78.8	105	4 US-09-220-407-169	Sequence 169, App
87	26	78.8	106	4 US-09-348-228-36	Sequence 36, Appl
88	26	78.8	106	4 US-09-248-796A-15619	Sequence 15619, A
89	26	78.8	107	4 US-09-543-681A-8265	Sequence 8265, Ap
90	26	78.8	121	1 US-08-481-377-20	Sequence 20, Appl
91	26	78.8	121	2 US-08-481-377-20	Sequence 20, Appl
92	26	78.8	121	3 US-09-153-733A-20	Sequence 20, Appl
93	26	78.8	121	3 US-08-946-092A-18	Sequence 18, Appl
94	26	78.8	121	3 US-09-172-062-18	Sequence 18, Appl
95	26	78.8	121	3 US-09-301-500D-18	Sequence 18, Appl
96	26	78.8	121	3 US-09-389-705-20	Sequence 20, Appl
97	26	78.8	121	5 PCT-US94-00666-20	Sequence 20, Appl
98	26	78.8	121	5 PCT-US94-00685-18	Sequence 18, Appl
99	26	78.8	122	1 US-08-581-559B-16	Sequence 16, Appl
100	26	78.8	122	1 US-08-455-559-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1

US-08-357-598-11
Sequence 11, Application US/08357598
Patent No. 5705625
GENERAL INFORMATION:
APPLICANT: Civin, Curt I.
APPLICANT: Small, Donald
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/357,598
FILING DATE: 15-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/033001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-357-598-11

Query Match 90.9%; Score 30; DB 1; Length 1100;

Best Local Similarity 71.4%; Pred. No. 4.3e+02; Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8

Db 228 PRRPYXL 234

RESULT 2

US-09-003-289-11
Sequence 11, Application US/09003289
Patent No. 5916792
GENERAL INFORMATION:
APPLICANT: Civin, Curt I.
APPLICANT: Small, Donald
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,289
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/357,598
FILING DATE: 15-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/033001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 amino acids
TYPE: amino acid
STRANDEDNESS: No. 5916792 Relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-003-289-11

Query Match

Best Local Similarity 90.9%; Score 30; DB 2; Length 1100;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8

Db 228 PRRPYXL 234

RESULT 3

PCT-US95-16435-11
Sequence 11, Application PCT/US9516435
GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
TITLE OF INVENTION: NOVEL PROTEIN TYROSINE KINASE, JAK3
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/16435
FILING DATE: 15-DEC-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/033001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1100 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-16435-11

Query Match 90.9%; Score 30; DB 5; Length 1100;
Best Local Similarity 71.4%; Pred. No. 4.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXRPLYL 8
Db 228 PSRPLYL 234

RESULT 4
US-09-543-681A-6625
; Sequence 6625, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6625
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6625

Query Match 87.9%; Score 29; DB 4; Length 323;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXRPLYL 8
Db 74 PLRPLYL 80

RESULT 5
US-09-489-039A-12281
; Sequence 12281, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12281
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12281

Query Match 87.9%; Score 29; DB 4; Length 323;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXRPLYL 8
Db 74 PRRPLYL 80

RESULT 6
US-09-543-681A-4495
; Sequence 4495, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:

APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543.681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 4495
; LENGTH: 328
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-4495

Query Match 87.9%; Score 29; DB 4; Length 328;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXRPLYL 8
Db 79 PMRPLYL 85

RESULT 7
US-09-252-991A-21222
; Sequence 21222, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21222
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21222

Query Match 87.9%; Score 29; DB 4; Length 332;
Best Local Similarity 71.4%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXRPLYL 8
Db 83 PKRPLYL 89

RESULT 8
US-08-946-994-17
; Sequence 17, Application US/08946994
; Patent No. 6210654
; GENERAL INFORMATION:
; APPLICANT: Ihle, James N.
; APPLICANT: Silvennoinen, Olli
; APPLICANT: Mitthun, Bruce A.
; APPLICANT: Quelle, Frederick W.
; TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine Signal
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.

ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/946,994
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/665,574
FILING DATE: 18-JUN-1996
APPLICATION NUMBER: 08/282,012
FILING DATE: 29-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/097,997
FILING DATE: 29-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/118,968
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0656.0370002/SLF/GKT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1098 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-946-994-17

Query Match 87.9%; Score 29; DB 3; Length 1098;
Best Local Similarity 71.4%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
DB 228 PRRPYAL 234

RESULT 9
US-08-665-574C-16
Sequence 16, Application US/08665574C
Patent No. 6136595
GENERAL INFORMATION:
APPLICANT: Ihle, James N.
APPLICANT: Silvenoinen, Olli
APPLICANT: Wiltuhm, Bruce A.
TITLE OF INVENTION: Jak Kinases and Regulation of Cytokine
TITLE OF INVENTION: Signal Transduction
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,574C
FILING DATE: 18-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/282,012

FILING DATE: 29-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/097,997
FILING DATE: 29-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/118,968
FILING DATE: 09-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Bugalsky, Lawrence B.
REGISTRATION NUMBER: 35,086
REFERENCE/DOCKET NUMBER: 0656.0370002/SLF/LBB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 1099 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-665-574C-16

Query Match 87.9%; Score 29; DB 3; Length 1099;
Best Local Similarity 71.4%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
DB 228 PRRPYAL 234

RESULT 10
US-09-949-016-10490
Sequence 10490, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10490
LENGTH: 1912
TYPE: PRT
ORGANISM: Human
US-09-949-016-10490

Query Match 87.9%; Score 29; DB 4; Length 1912;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
DB 1161 PRRPYAL 1167

RESULT 11
US-09-528-200-179
Sequence 179, Application US/09528200
Patent No. 6630570
GENERAL INFORMATION:
APPLICANT: LITKA, KAI
APPLICANT: BECKER, ANDREAS

APPLICANT: SEMMLER, WOLFHARD
APPLICANT: WEIDENMANN, BERTRAM
APPLICANT: HESSNIUS, CARSTEN
APPLICANT: VOLKMER-ENGERT, RUDOLF
APPLICANT: SCHNEIDER-MERGENER, JENS
APPLICANT: BHARGAVA, SARAH
TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
FILE REFERENCE: SCH-1731
CURRENT APPLICATION NUMBER: US/09/528,200
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: DE 199 17 713.9
PRIORITY FILING DATE: 1999-09-04
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 179
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-528-200-179

Query Match 84.8%; Score 28; DB 4; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYL 8
Db 1 PRRPYL 7

RESULT 12
US-09-484-318-7
Sequence 7, Application US/09484318
Patent No. 6180085
GENERAL INFORMATION:
APPLICANT: Achillefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorshow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: NOVEL DYES
FILE REFERENCE: DNA STRING
CURRENT APPLICATION NUMBER: US/09/484,318
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: THIS IS D-LYSINE.
OTHER INFORMATION: Description of Artificial Sequence: ANALOG OF
OTHER INFORMATION: NEUTROTENSIN
US-09-484-318-7

Query Match 84.8%; Score 28; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYL 8
Db 2 PRRPYL 8

RESULT 13
US-09-484-319-7
Sequence 7, Application US/09484319
Patent No. 6180086

GENERAL INFORMATION:
APPLICANT: Achillefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorshow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: NEW HYDROPHILIC CYANINE DYES
FILE REFERENCE: DNA STRING
CURRENT APPLICATION NUMBER: US/09/484,319
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: THIS IS D-LYSINE.
OTHER INFORMATION: Description of Artificial Sequence: ANALOG OF
OTHER INFORMATION: NEUTROTENSIN
US-09-484-319-7

Query Match 84.8%; Score 28; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYL 8
Db 2 PRRPYL 8

RESULT 14
US-09-484-320-7
Sequence 7, Application US/09484320
Patent No. 6180087
GENERAL INFORMATION:
APPLICANT: Achillefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorshow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: Tunable Indocyanine Dyes For Biomedical Applications
FILE REFERENCE: dnastring
CURRENT APPLICATION NUMBER: US/09/484,320
CURRENT FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: THIS IS D-LYSINE.
OTHER INFORMATION: Description of Artificial Sequence: ANALOG OF
OTHER INFORMATION: NEUTROTENSIN
US-09-484-320-7

Query Match 84.8%; Score 28; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYL 8
Db 2 PRRPYL 8

RESULT 15
US-09-484-321-7
Sequence 7, Application US/09484321
Patent No. 6183726
GENERAL INFORMATION:

```

; APPLICANT: Achillefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: VERSATILE HYDROPHILIC DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,321
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: THIS IS D-LYSINE.
; OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
; OTHER INFORMATION: NEUROTENSIN
US-09-484-321-7
```

```

Query Match      84.8%; Score 28; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 PRRPYXL 8
Db      2 PRRPYIL 8
```

```

RESULT 16
US-09-484-323-7
; Sequence 7, Application US/09484323
; Patent No. 6190641
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/484,323
; CURRENT FILING DATE: 2000-01-18
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: THIS IS D-LYSINE.
; OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
; OTHER INFORMATION: NEUROTENSIN
US-09-484-323-7
```

```

Query Match      84.8%; Score 28; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 PRRPYXL 8
Db      2 PRRPYIL 8
```

```

RESULT 17
US-09-325-769-8
; Sequence 8, Application US/09325769
; Patent No. 6217848
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
```

```

; APPLICANT: Dorshow, Richard B.
; APPLICANT: Bugaj, Joseph E.
; APPLICANT: Rajagopalan, Raghavan
; TITLE OF INVENTION: NOVEL CYANINE AND INDOCYANINE DYE BIOCONJUGATES FOR
; TITLE OF INVENTION: BIOMEDICAL APPLICATIONS
; FILE REFERENCE: 1668-286
; CURRENT APPLICATION NUMBER: US/09/325,769
; CURRENT FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: ATTY DOCKET 1668-284
; EARLIER FILING DATE: 1999-05-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This is D-lysine.
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Analog of
; OTHER INFORMATION: neurotensin.
US-09-325-769-8
```

```

Query Match      84.8%; Score 28; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 PRRPYXL 8
Db      2 PRRPYIL 8
```

```

RESULT 18
US-09-636-170-7
; Sequence 7, Application US/09636170
; Patent No. 6264919
; GENERAL INFORMATION:
; APPLICANT: Achillefu, Samuel
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Dorshow, Richard B
; APPLICANT: Bugaj, Joseph E.
; TITLE OF INVENTION: NOVEL INDOCYANINE DYES
; FILE REFERENCE: DNA STRING
; CURRENT APPLICATION NUMBER: US/09/636,170
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: THIS IS D-LYSINE.
; OTHER INFORMATION: Description of Artificial Sequence:ANALOG OF
; OTHER INFORMATION: NEUROTENSIN
US-09-636-170-7
```

```

Query Match      84.8%; Score 28; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 PRRPYXL 8
Db      2 PRRPYIL 8
```

```

RESULT 19
US-09-637-518-7
; Sequence 7, Application US/09637518
```

Patent No. 6264920
GENERAL INFORMATION:
APPLICANT: Achillefu, Samuel
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorshow, Richard B
APPLICANT: Bugaj, Joseph E.
TITLE OF INVENTION: Tunable Indocyanine Dyes for Biomedical Applications
FILE REFERENCE: dnaetng
CURRENT APPLICATION NUMBER: US/09/637,518
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: SITE
LOCATION: (1)
OTHER INFORMATION: THIS IS D-LYSINE.
OTHER INFORMATION: Description of Artificial Sequence: ANALOG OF
OTHER INFORMATION: NEUROTENSIN
US-09-637-518-7

Query Match 84.8%; Score 28; DB 3; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
Db 2 PRRPYXL 8

RESULT 20
US-09-528-200-178
Sequence 178, Application US/09528260
Patent No. 6630570
GENERAL INFORMATION:
APPLICANT: LICHA, KAI
APPLICANT: BECKER, ANDREAS
APPLICANT: SEMMLER, WOLFHARD
APPLICANT: WEIDENMANN, BERTRAM
APPLICANT: HESSNIUS, CARTSEN
APPLICANT: VOLKMER-ENGERT, RUDOLF
APPLICANT: SCHNEIDER-MERGENER, JENS
APPLICANT: BHARGAVA, SARAH
TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
FILE REFERENCE: SCH-1731
CURRENT APPLICATION NUMBER: US/09/528,200
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: DE 199 17 713.9
PRIOR FILING DATE: 1999-09-04
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 178
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-528-200-178

Query Match 84.8%; Score 28; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
Db 2 PRRPYXL 8

RESULT 21
US-09-863-971A-8
Sequence 8, Application US/09863971A
Patent No. 6641798
GENERAL INFORMATION:
APPLICANT: Achillefu, Samuel I.
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorshow, Richard B.
APPLICANT: Bugaj, Joseph E.
APPLICANT: Mallinckrodt Inc.
TITLE OF INVENTION: Tumor-Targeted Optical Contrast Agents
FILE REFERENCE: MRD-65
CURRENT APPLICATION NUMBER: US/09/863,971A
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/484,320
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(1)
OTHER INFORMATION: Xaa at location 1 represents D-Lys. Artificial sequence is
OTHER INFORMATION: completely synthesized.
US-09-863-971A-8

Query Match 84.8%; Score 28; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8
Db 2 PRRPYXL 8

RESULT 22
US-09-864-011A-8
Sequence 8, Application US/09864011A
Patent No. 6706254
GENERAL INFORMATION:
APPLICANT: Achillefu, Samuel I.
APPLICANT: Rajagopalan, Raghavan
APPLICANT: Dorshow, Richard B.
APPLICANT: Bugaj, Joseph E.
APPLICANT: Mallinckrodt Inc.
TITLE OF INVENTION: Receptor-Avid Exogenous Optical Contrast and Therapeutic
FILE REFERENCE: MRD-64
CURRENT APPLICATION NUMBER: US/09/864,011A
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 09/484,322
PRIOR FILING DATE: 2000-01-18
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 8
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)...(8)
OTHER INFORMATION: Xaa at location 1 represents D-Lys. Artificial sequence is
OTHER INFORMATION: completely synthesized.
US-09-864-011A-8

Query Match 84.8%; Score 28; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PRRPYXL 8

Db 2 PRRPYL 8

RESULT 23

US-09-978-725A-8
; Sequence 8, Application US/09978725A
; Patent No. 6761878
; GENERAL INFORMATION:
; APPLICANT: Achilleu, Samuel I.
; APPLICANT: Dorshow, Richard B.
; APPLICANT: Rajagopalan, Raghavan
; APPLICANT: Bugaj, Joseph E.
; APPLICANT: Mallinckrodt Inc.
; TITLE OF INVENTION: Pathological Tissue Detection and Treatment Employing
; TITLE OF INVENTION: Targeted Benzindole Optical Agents
; FILE REFERENCE: MRD-73
; CURRENT APPLICATION NUMBER: US/09/978,725A
; CURRENT FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Version 3.1
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (1)...(8)
; OTHER INFORMATION: Xaa at location 1 represents D-Lys. Artificial sequence is
; OTHER INFORMATION: completely synthesized.
US-09-978-725A-8

Query Match 84.8%; Score 28; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYL 8
Db 2 PRRPYL 8

RESULT 24
US-09-528-200-177
; Sequence 177, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: Licha, Kai
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 177
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-528-200-177

Query Match 84.8%; Score 28; DB 4; Length 9;

Best Local Similarity 71.4%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYL 8
Db 3 PRRPYL 9

RESULT 25
US-09-528-200-194
; Sequence 194, Application US/09528200
; Patent No. 6630570
; GENERAL INFORMATION:
; APPLICANT: Licha, Kai
; APPLICANT: BECKER, ANDREAS
; APPLICANT: SEMMLER, WOLFHARD
; APPLICANT: WEIDENMANN, BERTRAM
; APPLICANT: HESSNIUS, CARSTEN
; APPLICANT: VOLKMER-ENGERT, RUDOLF
; APPLICANT: SCHNEIDER-MERGENER, JENS
; APPLICANT: BHARGAVA, SARAH
; TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
; FILE REFERENCE: SCH-1731
; CURRENT APPLICATION NUMBER: US/09/528,200
; CURRENT FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: DE 199 17 713.9
; PRIOR FILING DATE: 1999-09-04
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 194
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-09-528-200-194

Query Match 84.8%; Score 28; DB 4; Length 10;
Best Local Similarity 71.4%; Pred. No. 8.9;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYL 8
Db 3 PRRPYL 9

RESULT 26
US-08-141-324-6
; Sequence 6, Application US/08141324
; Patent No. 5475097
; GENERAL INFORMATION:
; APPLICANT: Travis, James
; APPLICANT: Potempa, Jan S.
; APPLICANT: Barr, Philip J.
; APPLICANT: Pavloff, Nadine
; APPLICANT: Pike, Robert N.
; TITLE OF INVENTION: Lysine-specific Porphyromonas gingivalis
; TITLE OF INVENTION: Protease
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: CO
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Feider, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-141-324-6

Query Match 84.8%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PXPYPYL 8
Db 6 PRRPYIL 12

RESULT 27

US-08-541-902-6
Sequence 6, Application US/08541902
Patent No. 5707620

GENERAL INFORMATION:
APPLICANT: Travis, James
APPLICANT: Potempa, Jan S.
APPLICANT: Barr, Philip J.
APPLICANT: Pavloff, Nadine
APPLICANT: Pike, Robert N.
TITLE OF INVENTION: Lysozyme-specific Porphyromonas gingivalis
TITLE OF INVENTION: Protease
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: CO
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/541,902
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/141,324
FILING DATE: 21-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Feider, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 44-93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303-499-8080
TELEFAX: 303-499-8089
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-541-902-6

Query Match 84.8%; Score 28; DB 1; Length 12;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PXPYPYL 8
Db 6 PRRPYIL 12

RESULT 28

US-09-202-832-4
Sequence 4, Application US/09202832
Patent No. 6194190

GENERAL INFORMATION:
APPLICANT: IZU, Yukiko
APPLICANT: TANAKA, Tetsuki
APPLICANT: MIYAGI, Masaru
APPLICANT: TANIGAWA, Tetsuo
APPLICANT: TOMONO, Jun
APPLICANT: TSUNASAWA, Susumu
APPLICANT: KATO, Ikumobin
TITLE OF INVENTION: NOVEL AMINO-TERMINAL DEBLOCKING ENZYME
FILE REFERENCE: 1422-368P
CURRENT APPLICATION NUMBER: US/09/202,832
CURRENT FILING DATE: 1998-12-21
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Xaa = N-pyroglyutamyl-leucine
OTHER INFORMATION: Description of Artificial Sequence: Neurotensin
OTHER INFORMATION: manufactured by Peptide Institute, Inc.
US-09-202-832-4

Query Match 84.8%; Score 28; DB 3; Length 12;
Best Local Similarity 71.4%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 PXPYPYL 8
Db 6 PRRPYIL 12

RESULT 29

US-07-714-540-8
Sequence 8, Application US/07714540
Patent No. 5262521

GENERAL INFORMATION:
APPLICANT: Almqvist, Ronald G.
APPLICANT: Toll, Lawrence
TITLE OF INVENTION: ISOLATED ATRIAL PEPTIDE-DEGRADING
TITLE OF INVENTION: ENZYME AND NOVEL COMPOUNDS USEFUL AS INHIBITORS THEREOF
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Irell & Manella
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: California
COUNTRY: USA
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/714,540
FILING DATE: 19910607
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Dianne E.
REGISTRATION NUMBER: 31,292
REFERENCE/DOCKET NUMBER: 8500-0135.00
TELEPHONE: 415-327-7250
TELEFAX: 415-327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-714-540-8

Query Match 84.8%; Score 28; DB 1; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYL 8
DB 7 PRRPYL 13

RESULT 30
US-08-428-488-11
Sequence 11, Application US/08428488
Patent No. 5624894
GENERAL INFORMATION:
APPLICANT: BODOR, Nicholas S.
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
PEPTIDES BY SEQUENTIAL METABOLISM
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/428,488
FILING DATE: 27-APR-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Mary Katherine
REGISTRATION NUMBER: 26,254
REFERENCE/DOCKET NUMBER: 028724-087
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
NAME/KEY: Modified-site

LOCATION: 1
OTHER INFORMATION: /note= "Position 1 = p-Glu."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 13
OTHER INFORMATION: /note= "Position 13 = Leu-OH."

Query Match 84.8%; Score 28; DB 1; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYL 8
DB 7 PRRPYL 13

RESULT 31
US-08-747-137-117
Sequence 117, Application US/08747137
Patent No. 5945033
GENERAL INFORMATION:
APPLICANT: YEN, Richard C.K.
TITLE OF INVENTION: NON-CROSSLINKED PROTEIN PARTICLES FOR
THERAPEUTIC AND DIAGNOSTIC USE
NUMBER OF SEQUENCES: 184
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,137
FILING DATE: 12-NOV-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/212,546
FILING DATE: 14-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/069,831
FILING DATE: 01-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/959,560
FILING DATE: 13-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/641,720
FILING DATE: 15-JAN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 016197-000840US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "p-Glu"
US-08-747-137-117

Query Match 84.8%; Score 28; DB 2; Length 13;

Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPYXL 8
| | | | |
Db 7 PRRPYIL 13

RESULT 32

US-08-737-299A-1
Sequence 1, Application US/08737299A
Patent No. 5952464
GENERAL INFORMATION:
APPLICANT: MERTENS et al.
TITLE OF INVENTION: Labelled Peptide Compounds
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeffrey S. Boone
STREET: 675 McDonnell Blvd.
CITY: St. Louis
STATE: MO
COUNTRY: US
ZIP: 63134
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/737,299A
FILING DATE: 21-JUL-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02131
FILING DATE: 21-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Jeffrey S. Boone
REGISTRATION NUMBER: 29284
REFERENCE/DOCKET NUMBER: M0863-WO-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1 (314) 654-8955
TELEFAX: 1 (314) 654-3156
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "PYROGLUTAMIC ACID"
US-08-737-299A-1

Query Match 84.8%; Score 28; DB 2; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPYXL 8
| | | | |
Db 7 PRRPYIL 13

RESULT 33

US-09-334-254A-1
Sequence 1, Application US/09334254A
Patent No. 6194386
GENERAL INFORMATION:
APPLICANT: MERTENS et al.
TITLE OF INVENTION: Labelled Peptide Compounds
NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
ADDRESSEE: Jeffrey S. Boone
STREET: 675 McDonnell Blvd.
CITY: St. Louis
STATE: MO
COUNTRY: US
ZIP: 63134

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/334,254A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/737,299
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jeffrey S. Boone
REGISTRATION NUMBER: 29284
REFERENCE/DOCKET NUMBER: M0863-WO-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 1 (314) 654-8955
TELEFAX: 1 (314) 654-3156
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "PYROGLUTAMIC ACID"
US-09-334-254A-1

Query Match 84.8%; Score 28; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXPYXL 8
| | | | |
Db 7 PRRPYIL 13

RESULT 34

US-09-289-693-1
Sequence 1, Application US/09289693
Patent No. 6214790
GENERAL INFORMATION:
APPLICANT: Richelson, Elliott
APPLICANT: Cusack, Bernadette Marie
APPLICANT: Pang, Yuan-ping
APPLICANT: McCormick, Daniel J.
APPLICANT: Faud, Abdul
APPLICANT: Tyler, Beth Marie
APPLICANT: Boules, Mona
TITLE OF INVENTION: NEO-TRYPROPHAN
FILE REFERENCE: 07039/141001
CURRENT APPLICATION NUMBER: US/09/289,693
FILING DATE: 1999-04-09
EARLIER APPLICATION NUMBER: US 60/112,137
EARLIER FILING DATE: 1998-12-14
EARLIER APPLICATION NUMBER: US 60/098,119
EARLIER FILING DATE: 1998-08-27
EARLIER APPLICATION NUMBER: US 60/092,195
EARLIER FILING DATE: 1998-07-09
EARLIER APPLICATION NUMBER: US 60/081,356
EARLIER FILING DATE: 1998-04-10

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; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
; NAME/KEY: SITE
; LOCATION: (1)-(1)
; OTHER INFORMATION: Xaa = pyrrolidone carboxylic acid
US-09-289-693-1
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```
Query Match      84.8%; Score 28; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 PRRPYXL 8
        |||||
Db       7 PRRPYIL 13
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RESULT 35
US-09-355-869-2
; Sequence 2, Application US/09355869
; Patent No. 6312661
; GENERAL INFORMATION:
; APPLICANT: Reubi, Jean-Claude
; TITLE OF INVENTION: METHOD FOR THE DETECTION AND LOCALIZATION OF MALIGNANT
; TITLE OF INVENTION: HUMAN TUMOURS
; FILE REFERENCE: 1668-304
; CURRENT APPLICATION NUMBER: US/09/355, 869
; CURRENT FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: PCT/US98/01964
; PRIOR FILING DATE: 1998-02-02
; PRIOR APPLICATION NUMBER: EP 97200297.6
; PRIOR FILING DATE: 1997-02-03
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: This site is pyroglutamate.
US-09-355-869-2
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Query Match      84.8%; Score 28; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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```
QY      2 PRRPYXL 8
        |||||
Db       7 PRRPYIL 13
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RESULT 36
US-09-605-990-8
; Sequence 8, Application US/09605990
; Patent No. 6344551
; GENERAL INFORMATION:
; APPLICANT: Craig, A. Grey
; APPLICANT: Griffen, David
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Mackins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: Imperial, Juita
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Wagstaff, John D.
; APPLICANT: Layer, Richard T.
```

```
; APPLICANT: Jones, Robert M.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Salt Institute
; TITLE OF INVENTION: Conlulakin-G, Analogs Thereof and Uses Therefor
; FILE REFERENCE: Conlulakin-G
; CURRENT APPLICATION NUMBER: US/09/605, 990
; CURRENT FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/420, 797
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/130, 661
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 60/128, 561
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/105, 015
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Bos sp.
; NAME/KEY: PEPTIDE
; LOCATION: (1)
; OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.
US-09-605-990-8
```

```
Query Match      84.8%; Score 28; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 PRRPYXL 8
        |||||
Db       7 PRRPYIL 13
```

```
RESULT 37
US-09-420-797B-8
; Sequence 8, Application US/09420797B
; Patent No. 6369193
; GENERAL INFORMATION:
; APPLICANT: Craig, A. Grey
; APPLICANT: Griffen, David
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Walkins, Maren
; APPLICANT: Hillyard, David R.
; APPLICANT: Imperial, Juita
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Wagstaff, John D.
; APPLICANT: Layer, Richard T.
; APPLICANT: Jones, Robert M.
; APPLICANT: McCabe, R. Tyler
; APPLICANT: Cognetix, Inc.
; APPLICANT: University of Utah Research Foundation
; TITLE OF INVENTION: Conlulakin-G, Analogs Thereof and Uses Therefor
; FILE REFERENCE: Conlulakin-G
; CURRENT APPLICATION NUMBER: US/09/420, 797B
; CURRENT FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: US 60/130, 661
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 60/128, 561
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/105, 015
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Bos sp.
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FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)
OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.
US-09-420-797B-8

Query Match 84.8%; Score 28; DB 3; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYL 8
Db 7 PRRPYL 13

RESULT 38
US-09-605-991-8
Sequence 8, Application US/09605991
Patent No. 6489298
GENERAL INFORMATION:
APPLICANT: Craig, A. Grey
APPLICANT: Griffen, David
APPLICANT: Oliveira, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Hillyard, David R.
APPLICANT: Imperial, Julia
APPLICANT: Cruz, Lourdes J.
APPLICANT: Magstaf, John D.
APPLICANT: Layer, Richard T.
APPLICANT: Jones, Robert M.
APPLICANT: McCabe, R. Tyler
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Salk Institute
TITLE OF INVENTION: Contulakin-G, Analogs Thereof and Uses Therefor
FILE REFERENCE: Contulakin-G
CURRENT APPLICATION NUMBER: US/09/605,991
CURRENT FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US/09/420,797
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: US 60/130,661
PRIOR FILING DATE: 1999-04-23
PRIOR APPLICATION NUMBER: US 60/128,561
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/105,015
PRIOR FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 13
TYPE: PRT
ORGANISM: Bos sp.
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)
OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.
US-09-605-991-8

Query Match 84.8%; Score 28; DB 4; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYL 8
Db 7 PRRPYL 13

RESULT 39
US-09-609-534-8
Sequence 8, Application US/09609534
Patent No. 6525021
GENERAL INFORMATION:
APPLICANT: Craig, A. Grey

APPLICANT: Griffen, David
APPLICANT: Oliveira, Baldomero M.
APPLICANT: Watkins, Maren
APPLICANT: Hillyard, David R.
APPLICANT: Imperial, Julia
APPLICANT: Cruz, Lourdes J.
APPLICANT: Magstaf, John D.
APPLICANT: Layer, Richard T.
APPLICANT: Jones, Robert M.
APPLICANT: McCabe, R. Tyler
APPLICANT: Cognetix, Inc.
APPLICANT: University of Utah Research Foundation
APPLICANT: Salk Institute
TITLE OF INVENTION: Contulakin-G, Analogs Thereof and Uses Therefor
FILE REFERENCE: Contulakin-G
CURRENT APPLICATION NUMBER: US/09/609,534
CURRENT FILING DATE: 2000-06-30
EARLIER APPLICATION NUMBER: US 60/130,661
EARLIER FILING DATE: 1999-04-23
EARLIER APPLICATION NUMBER: US 60/128,561
EARLIER FILING DATE: 1999-04-09
EARLIER APPLICATION NUMBER: US 60/105,015
EARLIER FILING DATE: 1998-10-20
EARLIER APPLICATION NUMBER: US 09/420,797
EARLIER FILING DATE: 1999-10-19
EARLIER APPLICATION NUMBER: US 09/
EARLIER FILING DATE: 2000-06-29
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 8
LENGTH: 13
TYPE: PRT
ORGANISM: Bos sp.
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)
OTHER INFORMATION: Xaa at residue 1 is pyro-Glu.
US-09-609-534-8

Query Match 84.8%; Score 28; DB 4; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYL 8
Db 7 PRRPYL 13

RESULT 40
US-09-528-200-10
Sequence 10, Application US/09528200
Patent No. 6630570
GENERAL INFORMATION:
APPLICANT: Licha, Kai
APPLICANT: Beckler, Andreas
APPLICANT: Semmler, Wolfhard
APPLICANT: Weidenmann, Bertram
APPLICANT: Hessluis, Carsten
APPLICANT: Volkmmer-Engert, Rudolf
APPLICANT: Schneider-Mergener, Jens
APPLICANT: Bhargava, Sarah
TITLE OF INVENTION: SHORT-CHAIN PEPTIDE-DYE CONJUGATES AS CONTRAST MEDIA
FILE REFERENCE: SCH-1731
CURRENT APPLICATION NUMBER: US/09/528,200
CURRENT FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: DE 199 17 713.9
PRIOR FILING DATE: 1999-09-04
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 13
TYPE: PRT

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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: pglu
US-09-528-200-10

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Query Match      84.8%; Score 28; DB 4; Length 13;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      2 PRRPYL 8
        | ||| |
Db      7 PRRPYL 13

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Search completed: March 28, 2005, 08:39:01
 Job time : 46 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 28, 2005, 08:33:43 ; Search time 68 Seconds
(without alignments)
45.501 Million cell updates/sec

Title: US-10-036-918B-4

Perfect score: 33

Sequence: 1 XPRPYXL 8

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database: A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1980s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
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2	29	87.9	8 4	ABU31540 Amino aci
3	29	87.9	30 7	ADD15507 Predicted
4	29	87.9	53 4	AAH88000 Human Imm
5	29	87.9	70 4	AAU67965 Propionib
6	29	87.9	70 6	ABM64484 Propionib
7	29	87.9	74 4	AAU65129 Propionib
8	29	87.9	74 6	ABM61648 Propionib
9	29	87.9	157 6	ADA54863 Human pro
10	29	87.9	157 6	ABP71840 Human gly
11	29	87.9	216 8	ADG19768 G-Protein
12	29	87.9	281 6	ABU44862 Protein e
13	29	87.9	312 6	ABU26400 Protein e
14	29	87.9	314 6	ABP79282 N. gonorr
15	29	87.9	315 4	AAU35421 Haemophil
16	29	87.9	315 6	ABU39640 Protein e
17	29	87.9	315 6	ABU30234 Protein e
18	29	87.9	315 6	AAE30458 Haemophil
19	29	87.9	316 6	AAU36341 Pseudomon
20	29	87.9	316 6	ABU38589 Protein e
21	29	87.9	317 6	ABU39034 Protein e
22	29	87.9	317 6	ABU42211 Protein e
23	29	87.9	319 4	AAU34455 B. coli c
24	29	87.9	319 4	AAU38304 Salmoneil
25	29	87.9	319 6	ABU27909 Protein e

26	29	87.9	319 6	ABU48247 Protein e
27	29	87.9	319 6	ABU37156 Protein e
28	29	87.9	319 6	ABU49488 Protein e
29	29	87.9	319 6	ABU31682 Protein e
30	29	87.9	319 6	ABU50047 Protein e
31	29	87.9	319 6	ABU50047 Protein e
32	29	87.9	319 6	ABU47369 Protein e
33	29	87.9	319 6	ABU47369 Protein e
34	29	87.9	319 6	ABU15268 Protein e
35	29	87.9	319 7	ADD15500 Escherich
36	29	87.9	319 7	ADD15502 Escherich
37	29	87.9	320 6	ABU40545 Protein e
38	29	87.9	321 6	ABU23166 Protein e
39	29	87.9	323 6	ABU22657 Protein e
40	29	87.9	323 6	ABU19773 Protein e
41	29	87.9	323 7	ADF06340 Bacterial
42	29	87.9	323 7	ABO65764 Klebsiell
43	29	87.9	327 6	ABM67571 Phototrab
44	29	87.9	328 7	ADF04210 Bacterial
45	29	87.9	332 7	ABO72476 Pseudomon
46	29	87.9	432 5	AAE16173 Human G-P
47	29	87.9	450 3	AAE69894 Human rec
48	29	87.9	450 4	AAH85371 7 transme
49	29	87.9	450 4	AAE64208 Murine pr
50	29	87.9	450 4	AAE64209 Human G-P
51	29	87.9	450 8	AAU04586 Human G-P
52	29	87.9	450 8	ADH68221 Human G-P
53	29	87.9	504 4	ABE62417 Drosophil
54	29	87.9	504 7	AAE38187 Fruit fly
55	29	87.9	516 5	ABH06122 Human NS
56	29	87.9	783 4	ABH58228 Drosophil
57	29	87.9	783 8	ADH69518 Drosophil
58	29	87.9	1047 4	ABG29944 Novel hum
59	29	87.9	1098 4	AAE00358 Murine (J
60	29	87.9	1099 3	AAH35715 Murine Ja
61	29	87.9	1788 4	AAU00016 Human Ple
62	29	84.8	7 2	AAH71747 Neurotens
63	28	84.8	7 4	AAH45686 Neurotens
64	28	84.8	7 5	ADH68924 Synthetic
65	28	84.8	7 5	ADH68922 Synthetic
66	28	84.8	8 1	AAH40573 Sequence
67	28	84.8	8 1	AAH71385 Cyclic oc
68	28	84.8	8 2	AAH71751 Neurotens
69	28	84.8	8 2	AAH71749 Neurotens
70	28	84.8	8 4	AAH19958 Neurotens
71	28	84.8	8 4	AAH69157 Neurotens
72	28	84.8	8 4	AAH31541 Amino aci
73	28	84.8	8 4	AAH31525 Amino aci
74	28	84.8	8 4	AAH31531 Amino aci
75	28	84.8	8 4	AAH31542 Amino aci
76	28	84.8	8 4	AAH31528 Amino aci
77	28	84.8	8 4	AAH31528 Amino aci
78	28	84.8	8 4	AAH31533 Amino aci
79	28	84.8	8 4	AAH31533 Amino aci
80	28	84.8	8 4	AAH31530 Amino aci
81	28	84.8	8 4	AAH71702 Neurotens
82	28	84.8	8 4	AAH70516 Neurotens
83	28	84.8	8 4	AAH73426 Neurotens
84	28	84.8	8 4	AAU07325 Neurotens
85	28	84.8	8 4	AAH67686 Amino aci
86	28	84.8	8 4	AAE07139 Neurotens
87	28	84.8	8 4	AAH73432 Neurotens
88	28	84.8	8 4	AAH45683 Neurotens
89	28	84.8	8 4	AAH65289 Neurotens
90	28	84.8	8 5	AAU97459 Synthetic
91	28	84.8	8 5	ADH68915 Synthetic
92	28	84.8	8 5	ADH68917 Synthetic
93	28	84.8	8 6	ABU09471 Neurotens
94	28	84.8	8 6	ABR42469 Neurotens
95	28	84.8	8 6	ABR55708 Neurotens
96	28	84.8	8 6	ABR44103 Amino aci
97	28	84.8	8 7	ABR82876 Amino aci
98	28	84.8	9 2	AAH71755 Neurotens

[illegible][illegible]

Db 2 PARRYXL 8

RESULT 3
ADD15507
ID ADD15507 standard; peptide; 30 AA.

AC ADD15507;

DT 15-JAN-2004 (first entry)

DE Predicted epitopic region of the E.coli AccA protein (SeqID 72).

XX microbial; antimicrobial; membrane biosynthesis; pathogenic;

XX immunological response; vaccination; surface disinfectant;

KM personal hygiene application; food preservative; AccA;

XX acetyl-CoA carboxylase carboxyl transferase subunit alpha; epitope.

OS Escherichia coli.

PN WO2003025007-A2.

PD 27-MAR-2003.

PF 20-SEP-2002; 2002WO-CA001428.

PR 21-SEP-2001; 2001US-0323992P.

PR 21-SEP-2001; 2001US-0324152P.

PR 25-SEP-2001; 2001US-0324682P.

PR 26-OCT-2001; 2001US-0339924P.

PR 29-OCT-2001; 2001US-0350973P.

PR 30-OCT-2001; 2001US-0340924P.

PR 27-NOV-2001; 2001US-0333666P.

PR 18-DEC-2001; 2001US-0341732P.

PR 18-DEC-2001; 2001US-0341776P.

PR 19-DEC-2001; 2001US-0341949P.

PA (AFFI-) AFFINIUM PHARM INC.

PI Edwards A, Dharamsi A, Vedadi M, Alam WZ, Awrey D, Beattie B;

PI Domagala M, Houston S, Kanagarajah D, Nethery K, Ng I, Mansoury K;

PI McDonald M, Pinder B, Viola C, Wrezel O;

DR WPI; 2003-468119/44.

PT Novel crystallized recombinant polypeptides from Staphylococcus aureus,

PT Streptococcus pneumoniae and Escherichia coli and which are involved in

PT membrane biosynthesis, useful as targets for pathogenic bacteria.

PS Disclosure; SEQ ID NO 72; 325bp; English.

XX This invention relates to the structural and functional characterisation

XX of microbial polypeptides from Staphylococcus aureus (S. aureus),

XX Streptococcus pneumoniae (S. pneumoniae) and Escherichia coli (E. coli)

XX that provide novel antimicrobial targets. Specifically, it refers to

XX polypeptides that are involved in membrane biosynthesis, which play a

XX critical role in the life cycle and viability of their pathogenic species

XX of origin, and hence provide valuable drug targets. Furthermore, the

XX characterisation describes modified version of these proteins that facilitate

XX fusion proteins. These proteins provide structural and functional

XX information to aid the discovery of therapeutic molecules to treat

XX disorders associated with a particular pathogenic species. As such, they

XX are useful for inducing an immunological response in an individual and as

XX an antigen for vaccination purposes. The polypeptides are also useful for

XX developing antimicrobial agents for use as surface disinfectants,

XX personal hygiene applications and as food preservatives or in treating

XX food products to eliminate potential pathogens. This peptide sequence is

XX a predicted epitopic sequence of the E. coli AccA protein of the

XX invention.

XX Sequence 30 AA;

Query Match 87.9%; Score 29; DB 7; Length 30;
Best Local Similarity 71.4%; Pred. NO. 58;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2 PARRYXL 8

ADD15507
ID ADD15507 standard; protein; 53 AA.

AC ADD15507;

DT 07-NOV-2001 (first entry)

DE Human immune/haematopoietic antigen SEQ ID NO:15593.

XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;

XX cytosolic; gene therapy; vaccine; metastasis.

OS Homo sapiens.

PN WO200157182-A2.

PD 09-AUG-2001.

PF 17-JAN-2001; 2001WO-US001354.

PR 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184664P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 07-JUL-2000; 2000US-0216880P.

PR 11-JUL-2000; 2000US-0217487P.

PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.

PR 26-JUL-2000; 2000US-0220963P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225265P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 14-AUG-2000; 2000US-0225757P.

PR 14-AUG-2000; 2000US-0225758P.

PR 14-AUG-2000; 2000US-0225759P.

PR 18-AUG-2000; 2000US-0226279P.

PR 22-AUG-2000; 2000US-0226681P.

PR 22-AUG-2000; 2000US-0226682P.

PR 22-AUG-2000; 2000US-0227182P.

PR 23-AUG-2000; 2000US-0227009P.

PR 30-AUG-2000; 2000US-0228924P.

PR 01-SEP-2000; 2000US-0229287P.

PR 01-SEP-2000; 2000US-0229343P.

PR 01-SEP-2000; 2000US-0229344P.

PR 01-SEP-2000; 2000US-0229345P.

PR 05-SEP-2000; 2000US-0229509P.

PR 05-SEP-2000; 2000US-0229513P.

PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236337P.
PR 29-SEP-2000; 2000US-0236357P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-024617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249209P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.

PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249255P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251968P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
PA Rosen CA, Barash SC, Ruben SM;
PI WPI: 2001-483426/52.
XX N-PSDB; AAK60781.
DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and metastasis.
XX Claim 11; SEQ ID NO 15593; 3071pp + Sequence Listing; English.
PS
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 53 AA;
Query Match 87.9%; Score 29; DB 4; Length 53;
Best Local Similarity 85.7%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 1;
QY 2 PXRPRYL 8
Db 44 PXRPRYL 50
RESULT 5
AAU67965
ID AAU67965 standard; protein; 70 AA.
XX
AC AAU67965;
XX
DT 27-FEB-2002 (first entry)
DE Propionibacterium acnes immunogenic protein #28861.
XX

KM SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KM uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KM inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KM dermatological; osteopathic; neuroprotectant.
 OS Propionibacterium acnes.
 XX WO200181581-A2.
 XX
 XX 01-NOV-2001.
 PD
 XX 20-APR-2001; 2001WO-US012865.
 XX
 XX 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L'maisonneuve J, Zhang Y, Jen S, Carter D;
 DR WPI; 2001-616774/71.
 DR N-PSDB; AAS59773.
 XX
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 PS
 XX Example 1; SEQ ID NO 29160; 1069pp; English.
 CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC therefore treat P. acnes infections. The antibodies may also be used as
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 70 AA;
 QY Query Match 87.9%; Score 29; DB 4; Length 70;
 Db Best Local Similarity 71.4%; Pred. NO. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 2 PXRPRYXL 8
 38 PYRPRYSL 44
 RESULT 6
 ID ABM64484 standard; protein; 70 AA.
 AC ABM64484;
 XX
 XX 20-OCT-2003 (first entry)
 DT
 XX Propionibacterium acnes predicted ORF-encoded polypeptide #29160.
 DE
 XX

KM Acne vulgaris; antiseborrheic; dermatological; antibacterial;
 KM immunostimulant; immune response; vaccine.
 XX
 OS Propionibacterium acnes.
 XX WO2003033515-A1.
 XX
 XX 24-APR-2003.
 PD
 XX 11-OCT-2002; 2002WO-US032727.
 XX
 XX 15-OCT-2001; 2001US-00978825.
 XX
 XX (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAM, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Vailleve-Douglases J;
 XX
 XX WPI; 2003-381789/36.
 DR N-PSDB; ACF64702.
 DR
 XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 PS
 XX Example 1; SEQ ID NO 29160; 1481pp; English.
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polynucleotides encoded by the polynucleotides (ABM35624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 70 AA;
 QY Query Match 87.9%; Score 29; DB 6; Length 70;
 Db Best Local Similarity 71.4%; Pred. NO. 1.4e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 2 PXRPRYXL 8
 38 PYRPRYSL 44
 RESULT 7
 ID AAU65129 standard; protein; 74 AA.
 AC AAU65129;
 XX
 XX
 XX

DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #26025.
 XX
 KM SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KM uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KM inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KM dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US012865.
 XX
 PR 21-APR-2000; 2000US-0199047P.
 PR 02-JUN-2000; 2000US-0208841P.
 PR 07-JUL-2000; 2000US-0216747P.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhatia A;
 PI L' Maisonneuve J, Zhang Y, Jen S, Carter D;
 XX
 DR N-PSDB; AAS59660.
 DR WPI; 2001-616774/71.
 PT
 PT Propionibacterium acnes polypeptides and nucleic acids useful for
 PT vaccinating against and diagnosing infections, especially useful for
 PT treating acne vulgaris.
 XX
 PS Example 1; SEQ ID NO 26324; 1069pp; English.
 XX
 CC Sequences AAU93105-AAU68017 represent Propionibacterium acnes immunogenic
 CC polypeptides. The proteins and their associated DNA sequences are used in
 CC the treatment, prevention and diagnosis of medical conditions caused by
 CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,
 CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.
 CC P. acnes is also involved in infections of bone, joints and the central
 CC nervous system, however it is particularly involved in the inflammatory
 CC lesions associated with acne vulgaris. A method for detecting the
 CC presence or absence of P. acnes in a patient comprises contacting a
 CC sample with a binding agent that binds to the proteins of the invention
 CC and determining the amount of bound protein in the sample. The
 CC polypeptides may be used as antigens in the production of antibodies
 CC specific for P. acnes proteins. These antibodies can be used to
 CC downregulate expression and activity of P. acnes polypeptides and
 CC diagnostic agents for determining P. acnes presence, for example, by
 CC enzyme linked immunosorbent assay (ELISA). Note: The sequence data for
 CC this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 74 AA;
 Query Match 87.9%; Score 29; DB 4; Length 74;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXPXYXL 8
 Db 38 PYRPSYL 44
 RESULT 8
 ABM61648
 ID ABM61648 standard; protein, 74 AA.
 XX
 AC ABM61648;
 XX

DT 20-OCT-2003 (first entry)
 XX
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #26324.
 XX
 KM Acne vulgaris; anti-seborrheic; dermatological; antibacterial;
 KM immunostimulant; immune response; vaccine.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO2003033515-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 11-OCT-2002; 2002WO-US032727.
 XX
 PR 15-OCT-2001; 2001US-00978825.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Mitcham JL, Skeiky YAM, Persing DH, Bhatia A, Maisonneuve JL;
 PI Zhang Y, Wang S, Jen S, Lodes MJ, Benson DR, Jones R, Carter D;
 PI Barth B, Valiève-Douglas J;
 XX
 DR WPI; 2003-381789/36.
 DR N-PSDB; ACF64589.
 XX
 PT New Propionibacterium acnes polypeptides and polynucleotides encoding the
 PT polypeptide, useful for diagnosing, preventing or treating acne vulgaris,
 PT or for stimulating an immune response specific for a P. acnes protein.
 XX
 PS Example 1; SEQ ID NO 26324; 1481pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (ACF64435-ACF64733)
 CC encoding a Propionibacterium acnes protein. The invention also relates to
 CC polypeptides encoded by the polynucleotides (ABM5624-ABM64536) and to
 CC immunogenic fragments of P. acnes polypeptides. The invention
 CC additionally encompasses expression vectors and host cells comprising a
 CC polynucleotide of the invention; antibodies against polypeptides of the
 CC invention; fusion proteins comprising a polypeptide of the invention; a
 CC method for stimulating an immune response specific for a P. acnes
 CC polypeptide and an isolated T cell population comprising T cells prepared
 CC via this method; a vaccine composition (comprising P. acnes polypeptides,
 CC polynucleotides, antibodies, fusion proteins, T cell populations, or
 CC antigen-presenting cells that express the polypeptide); a method and kit
 CC for detecting or determining the presence or absence of P. acnes in a
 CC patient; and a method for inhibiting the development of P. acnes in a
 CC patient. The P. acnes polypeptides, polynucleotides, antibodies, fusion
 CC proteins, T cell populations or antigen-presenting cells that express the
 CC polypeptides are useful for diagnosing, preventing or treating acne
 CC vulgaris, or for stimulating an immune response specific for a P. acnes
 CC protein. The polynucleotides can also be used as probes or primers for
 CC nucleic acid hybridisation. The vaccine composition is useful for the
 CC stimulation of an immune response against P. acnes, or for treating acne,
 CC and the kit is useful for performing a diagnostic assay. The present
 CC sequence represents a polypeptide predicted to be encoded by an ORF (open
 CC reading frame) contained within the P. acnes polynucleotides of the
 CC invention. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 74 AA;
 Query Match 87.9%; Score 29; DB 6; Length 74;
 Best Local Similarity 71.4%; Pred. No. 1.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXPXYXL 8
 Db 38 PYRPSYL 44
 RESULT 9
 ADAS4863

ID ADA54863 standard; protein; 157 AA.
XX
AC ADA54863;
XX
XX
DT 20-NOV-2003 (first entry)
XX
DE Human protein, SEQ ID 2431.
XX
KM Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KM Gene Therapy; human; secretory protein; membrane proteins; cancer;
KM inflammatory disease; osteoporosis; neurological disease.
XX
OS Homo sapiens.
XX
PN EPI293569-A2.
XX
PD 19-MAR-2003.
XX
PF 21-MAR-2002; 2002EP-00006586.
XX
PR 14-SEP-2001; 2001JP-00328381.
PR 24-JAN-2002; 2002US-0350435P.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuno Y;
XX
DR WPI; 2003-395539/38.
DR N-PSDB; ADA53224.
XX
PT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
PS Claim 14; SEQ ID NO 2431; 205pp; English.
XX
CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX
SQ Sequence 157 AA;
XX
Query Match 87.9%; Score 29; DB 6; Length 157;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 2 PXRPRYXL 8
Db 43 PNRPRYTL 49
XX
RESULT 10
ABP71840
ID ABP71840 standard; protein; 157 AA.
XX
AC ABP71840;
XX
DT 23-APR-2003 (first entry)
XX
DE Human glycosyl-phosphatidyl inositol polyase 17.27.
XX
KM Human; glycosyl-phosphatidyl inositol polyase 17.27; immunity disorder;
KM enzyme.
XX
OS Homo sapiens.
XX
PN CNI355221-A.
XX

PD 26-JUN-2002.
XX
XX 24-NOV-2000; 2000CN-00127566.
PF
XX
XX 24-NOV-2000; 2000CN-00127566.
PR
XX
XX (UYFU-) UNIV FUDAN.
XX
XX Mao Y, Xie Y;
XX
PI WPI; 2003-000146/01.
XX
DR N-PSDB; ABZ69861.
XX
PT polypeptide-human glycosyl-phosphatidyl inositol polyase and
PT polynucleotide for coding it.
XX
XX
PS Claim 1; Page 28 (Disclosure); 35pp; Chinese.
XX
CC The invention relates to the novel human glycosyl-phosphatidyl inositol
CC polyase 17.27, and the polynucleotide encoding it. The polypeptide is
CC useful in treating diseases such as immunity disorders. The antagonist
CC against this polypeptide and its therapeutic action, and the application
CC of the polynucleotide are also disclosed. The present sequence represents
CC the human glycosyl-phosphatidyl inositol polyase 17.27 of the invention
XX
SQ Sequence 157 AA;
XX
Query Match 87.9%; Score 29; DB 6; Length 157;
Best Local Similarity 71.4%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
Qy 2 PXRPRYXL 8
Db 43 PNRPRYTL 49
XX
RESULT 11
ADG19768
ID ADG19768 standard; protein; 216 AA.
XX
AC ADG19768;
XX
DT 26-FEB-2004 (first entry)
XX
DE G-protein coupled receptor domain related consensus seq id 106.
XX
KM cyostatic; nephroretropic; antiinflammatory; cardiac; respiratory;
KM gastrointestinal; neuroprotective; angiogenesis stimulator; gene therapy;
KM 18636; 2466; 43338; 1983; 52881; 2398; 45449; 50289; 52872; 26308;
KM cellular proliferative disorder; brain disorder; renal disorder;
KM kidney disorder; inflammatory disorder; cardiovascular disorder;
KM liver disorder; intestinal disorder; respiratory disorder;
KM angiogenic disorder; human; G protein coupled receptor; GPCR;
KM protein domain.
XX
XX Unidentified.
XX
XX US2003215860-A1.
PN
XX
PD 20-NOV-2003.
XX
PF 03-APR-2003; 2003US-00407079.
XX
PR 29-FEB-2000; 2000US-0186059P.
PR 24-MAR-2000; 2000US-0191845P.
PR 22-MAY-2000; 2000US-0206019P.
PR 17-NOV-2000; 2000US-00715790.
PR 28-FEB-2001; 2001US-00796338.
PR 22-MAY-2001; 2001US-00863200.
PR 22-AUG-2001; 2001US-0314041P.
PR 22-AUG-2001; 2001US-0314185P.
PR 21-AUG-2002; 2002US-00225094.
PR 22-AUG-2002; 2002US-00226102.
PR

PR 15-OCT-2002; 2002US-00272417.
 PR 29-OCT-2002; 2002US-00282837.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 PI Gluckmann MA, Sijos-Santiago I, Carroll JM, Galvin KM;
 XX
 DR WPI; 2004-010777/01.
 XX
 PT New nucleic acid or polypeptide 18636, 2466, 43238, 1983, 52881, 2398,
 PT 45449, 50289, 52872 or 26908; useful in preparing a composition for
 PT treating e.g., cellular proliferative, brain, kidney, inflammatory or
 PT angiogenic disorder.
 XX
 PS Disclosure; SEQ ID NO 106; 163pp; English.
 XX
 CC The invention describes a new isolated 18636, 2466, 43238, 1983, 52881,
 CC 2398, 45449, 50289, 52872 or 26908 nucleic acid molecule comprising: a
 CC sequence comprising 939-3489 bp or its fragment comprising at least 15
 CC nucleotides; a sequence encoding a polypeptide comprising a sequence
 CC having 223-852 amino acids, or its allelic variant or fragment comprising
 CC at least 15 contiguous amino acids; or a sequence that hybridizes with
 CC (1) under stringent conditions. The nucleic acid or polypeptide is useful
 CC in preparing a composition for treating a disorder characterised by
 CC aberrant 18636, 2466, 43238, 1983, 52881, 2398, 45449, 50289, 52872 or
 CC 26908 activity e.g., cellular proliferative, brain, renal, kidney,
 CC inflammatory, cardiovascular, liver, intestinal, respiratory or
 CC angiogenic disorder. This is the amino acid sequence of a human G-protein
 CC coupled receptor 32 (GPCR32) polypeptide used in the characterisation of
 CC novel human G-protein coupled receptor 26908.
 XX
 SQ Sequence 216 AA;
 XX
 QY 2 PXRPLYL 8
 DB 191 PDREYSL 197
 XX
 Query Match 87.9%; Score 29; DB 8; Length 216;
 Best Local Similarity 71.4%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 12
 ABU44862
 ID ABU44862 standard; protein; 281 AA.
 XX
 AC ABU44862;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #30389.
 XX
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Salmonella paratyphi.
 XX
 PN WO200277183-A2.
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948893.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362659P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wei D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX

DR WPI; 2003-029926/02.
 DR N-PSDB; ACA48732.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 72786; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 281 AA;
 XX
 QY 2 PXRPLYL 8
 DB 33 PDREYTL 39
 XX
 Query Match 87.9%; Score 29; DB 6; Length 281;
 Best Local Similarity 71.4%; Pred. No. 6e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 13
 ABU26400
 ID ABU26400 standard; protein; 312 AA.
 XX
 AC ABU26400;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #11927.
 XX
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Campylobacter jejuni.
 XX
 PN WO200277183-A2.
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 XX

PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA30270.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 54324; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 312 AA;
 Query Match 87.9%; Score 29; DB 6; Length 312;
 Best Local Similarity 71.4%; Pred. No. 6.7e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PRRPYXL 8
 DB 60 PDRPYAL 66
 XX
 RESULT 14
 ABP79282
 ID ABP79282 standard; protein; 314 AA.
 XX
 AC ABP79282;
 XX
 DT 07-MAR-2003 (first entry)
 XX
 DE N. gonorrhoeae amino acid sequence SEQ ID 5094.
 XX
 KW Antibacterial; infection; vaccine; gene therapy.

XX
 OS Neisseria gonorrhoeae.
 XX
 PN WO200279243-A2.
 XX
 PD 10-OCT-2002.
 XX
 PP 12-FEB-2002; 2002WO-IB002069.
 XX
 PR 12-FEB-2001; 2001GB-00003424.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Fontana MR, Pizsa M, Massignani V, Monaci E;
 XX
 DR WPI; 2003-058415/05.
 DR N-PSDB; ABZ40252.
 XX
 PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a
 PT medicament for treating or preventing N. gonorrhoeae infection.
 XX
 PS Disclosure; Page 561; 815pp; English.
 XX
 CC The present invention relates to proteins from Neisseria gonorrhoeae.
 CC Also disclosed are the nucleic acid molecules encoding the proteins and
 CC antibodies that specifically bind to the proteins. The composition
 CC comprising the protein, nucleic acid or antibody is useful for the
 CC manufacture of a medicament for treating or preventing N. gonorrhoeae
 CC infection, this may be in the form of a vaccine or gene therapy.
 CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
 CC molecules of the invention
 XX
 SQ Sequence 314 AA;
 Query Match 87.9%; Score 29; DB 6; Length 314;
 Best Local Similarity 71.4%; Pred. No. 6.7e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PRRPYXL 8
 DB 62 PDRPYTL 68
 XX
 RESULT 15
 AAU35421
 ID AAU35421 standard; protein; 315 AA.
 XX
 AC AAU35421;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Haemophilus influenzae cellular proliferation protein #62.
 XX
 KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
 KW antibacterial; drug design.
 XX
 OS Haemophilus influenzae.
 XX
 PN WO200170955-A2.
 XX
 PD 27-SEP-2001.
 XX
 PP 21-MAR-2001; 2001WO-US009180.
 XX
 PR 21-MAR-2000; 2000US-0191078P.
 PR 23-MAY-2000; 2000US-0206848P.
 PR 26-MAY-2000; 2000US-0207727P.
 PR 23-OCT-2000; 2000US-0242578P.
 PR 27-NOV-2000; 2000US-0253625P.
 PR 22-DEC-2000; 2000US-0257931P.
 PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.

XX Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
 PI Yamamoto RT, Xu HH;
 XX WPI; 2001-611495/70.
 DR N-PSDB; AAS53280.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 11014; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes,
 CC themselves and the encoded proteins. The prokaryotes used are Escherichia
 CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
 CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 315 AA;
 QY
 Db 2 PXRPPYXL 8
 66 PNRPPYTL 72

RESULT 16
 ABU39640
 ID ABU39640 standard; protein; 315 AA.
 XX
 AC ABU39640;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #25167.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Pseudomonas putida.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

DR WPI; 2003-029926/02.
 DR N-PSDB; ACA43510.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 67564; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than S. aureus, S. typhimurium,
 CC K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 315 AA;
 QY
 Db 2 PXRPPYXL 8
 67 PRRPPYTL 73

RESULT 17
 ABU30234
 ID ABU30234 standard; protein; 315 AA.
 XX
 AC ABU30234;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #15761.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Haemophilus influenzae.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
XX (ELIT-.) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
XX WPI: 2003-029926/02.
DR N-PSDB; ACA34104.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 58158; 1766pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 315 AA;
SQ

Query Match 87.9%; Score 29; DB 6; Length 315;
Best Local Similarity 71.4%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 PXRPYXL 8
| | | | |
Db 66 PNRPYTL 72

RESULT 18
AAE30458
ID AAE30458 standard; protein; 315 AA.
XX
XX AAE30458;
AC
XX
XX 24-FEB-2003 (first entry)
DT
XX
DE Haemophilus influenza acetyl coA carboxylase protein.
XX
KW Virulence; veterinary; infection; pneumonia; antimicrobial drug; vaccine;

KW antibiotic; gene therapy; antibacterial; acetyl coA carboxylase; enzyme.
XX
XX Haemophilus influenzae.
XX
XX WO200277020-A2.
XX
XX 03-OCT-2002.
PD
XX
XX 18-MAR-2002; 2002WO-GB001305.
PF
XX
XX 22-MAR-2001; 2001GB-00007234.
PR 23-MAR-2001; 2001GB-00007360.
XX
XX (ISIS-) ISIS INNOVATION LTD.
PA
PI Herbert MA, Deadman ME, Hood DW, Moxon ER;
XX
XX WPI: 2003-029913/02.
DR N-PSDB; AAD47826.
XX
XX New virulence gene from Hemophilus influenzae, useful for producing
PT vaccines or antibiotics for preventing or treating pneumonia.
PT
XX
XX Claim 4; Page 30-31; 132pp; English.
PS
XX
XX The present invention relates to Hemophilus influenzae virulence genes
CC and proteins encoded by them. The microorganisms or the peptides of the
CC invention are useful for manufacturing a medicament for treating
CC (veterinary) or preventing a condition associated with *H. influenzae*
CC infection, particularly pneumonia or for identifying an antimicrobial
CC drug. Sequences of the invention are useful in the production of vaccines
CC or antibiotics to prevent or treat *H. influenzae* infection. They are also
CC used in gene therapy. The present sequence is *H. influenzae* acetyl coA
CC carboxylase protein
XX
XX Sequence 315 AA;
SQ

Query Match 87.9%; Score 29; DB 6; Length 315;
Best Local Similarity 71.4%; Pred. No. 6.7e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 PXRPYXL 8
| | | | |
Db 66 PNRPYTL 72

RESULT 19
AAU36341
ID AAU36341 standard; protein; 316 AA.
XX
XX AAU36341;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Pseudomonas aeruginosa cellular proliferation protein #331.
DE
XX
KW Antisense; prokaryotic cellular proliferation protein; antibiotic;
KW antibacterial; drug design.
XX
XX Pseudomonas aeruginosa.
OS
XX
XX WO200170955-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US009180.
PF
XX
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.

PR 16-FEB-2001; 2001US-0269308P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ,
 PI Yamamoto RT, Xu HH;
 XX
 DR WPI; 2001-611495/70.
 DR N-PSDB; AAS54200.
 XX
 PT New polynucleotides for the identification and development of
 PT antibiotics, comprise sequences of antisense nucleic acids.
 XX
 PS Example 3; SEQ ID NO 11934; 511pp; English.
 XX
 CC The invention relates to antisense inhibitors of genes essential to
 CC prokaryotic cellular proliferation, their use in identifying the genes,
 CC their use in the discovery of novel antibiotics, the essential genes
 CC themselves and the encoded proteins. The prokaryotes used are *Bacteriella*
 CC coli, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*,
 CC *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also
 CC useful for the identification of potential new targets for antibiotic
 CC development. The antisense nucleic acids can also be used to identify
 CC proteins used in proliferation, to express these proteins, and to obtain
 CC antibodies capable of binding to the expressed proteins. The proteins can
 CC be used to screen compounds in rational drug discovery programmes. The
 CC antisense nucleic acid sequence is also useful to screen for homologous
 CC nucleic acids which are required for cell proliferation in a wide variety
 CC of organisms. The present sequence represents an essential prokaryotic
 CC cellular proliferation protein. Note: The sequence data for this patent
 CC did not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 316 AA;
 Query Match 87.9%; Score 29; DB 4; Length 316;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PKRPTXL 8
 Db 67 PKRPTTL 73
 XX
 RESULT 20
 ABU38589
 ID ABU38589 standard; protein; 316 AA.
 XX
 AC ABU38589;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by prokaryotic essential gene #24116.
 XX
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Pseudomonas aeruginosa*.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 06-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;
 XX
 DR WPI; 2003-029926/02.
 DR N-PSDB; ACA42459.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 66513; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 316 AA;
 Query Match 87.9%; Score 29; DB 6; Length 316;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PKRPTXL 8
 Db 67 PKRPTTL 73
 XX
 RESULT 21
 ABU39034
 ID ABU39034 standard; protein; 317 AA.
 XX
 AC ABU39034;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by prokaryotic essential gene #24561.
 XX
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Pasteurella multocida*.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX

PF 21-MAR-2002; 2002WO-US009107.
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.
 PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA42904.
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 PS Claim 25; SEQ ID NO 66958; 1766pp; English.
 XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 317 AA;
 QY Query Match 87.9%; Score 29; DB 6; Length 317;
 Db Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DE Protein encoded by Prokaryotic essential gene #27738.
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX Pseudomonas syringae.
 OS WO200277183-A2.
 XX
 XX 03-OCT-2002.
 PD
 PF 21-MAR-2002; 2002WO-US009107.
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX (ELIT-) ELITRA PHARM INC.
 PA Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 DR N-PSDB; ACA46081.
 XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 PS Claim 25; SEQ ID NO 70135; 1766pp; English.
 XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 317 AA;
 QY Query Match 87.9%; Score 29; DB 6; Length 317;
 Db Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
RESULT 23
ID AU34455 standard; protein, 319 AA.
XX
XX AAU34455;
XX
DT 14-FEB-2002 (first entry)
XX
XX E. coli cellular proliferation protein #36.
DE
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Escherichia coli.
OS
XX WO200170955-A2.
PN
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US009180.
PF
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX Haselbeck R, Ohlsen KU, Zykind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
DR N-PSDB; AAS52314.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 10048; 511p; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 319 AA;
SQ
Query Match 87.9%; Score 29; DB 4; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 24
ID AU38304 standard; protein, 319 AA.
XX
XX AU38304;
XX
DT 14-FEB-2002 (first entry)
XX
XX Salmonella typhi cellular proliferation protein #195.
DE
XX Antisense; prokaryotic cellular proliferation protein; antibiotic;
KM antibacterial; drug design.
XX
XX Salmonella typhi.
OS
XX WO200170955-A2.
PN
XX 27-SEP-2001.
PD
XX
XX 21-MAR-2001; 2001WO-US009180.
PF
XX 21-MAR-2000; 2000US-0191078P.
PR 23-MAY-2000; 2000US-0206848P.
PR 26-MAY-2000; 2000US-0207727P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX
XX (ELIT-) ELITRA PHARM INC.
PA
XX Haselbeck R, Ohlsen KU, Zykind JW, Wall D, Trawick JD, Carr GJ;
PI Yamamoto RT, Xu HH;
PI WPI; 2001-611495/70.
DR N-PSDB; AAS56163.
XX
XX New polynucleotides for the identification and development of
PT antibiotics, comprise sequences of antisense nucleic acids.
XX
XX Example 3; SEQ ID NO 13897; 511p; English.
XX
XX The invention relates to antisense inhibitors of genes essential to
CC prokaryotic cellular proliferation, their use in identifying the genes,
CC their use in the discovery of novel antibiotics, the essential genes
CC themselves and the encoded proteins. The prokaryotes used are Escherichia
CC coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae,
CC Pseudomonas aeruginosa and Enterococcus faecalis. The invention is also
CC useful for the identification of potential new targets for antibiotic
CC development. The antisense nucleic acids can also be used to identify
CC proteins used in proliferation, to express these proteins, and to obtain
CC antibodies capable of binding to the expressed proteins. The proteins can
CC be used to screen compounds in rational drug discovery programmes. The
CC antisense nucleic acid sequence is also useful to screen for homologous
CC nucleic acids which are required for cell proliferation in a wide variety
CC of organisms. The present sequence represents an essential prokaryotic
CC cellular proliferation protein. Note: The sequence data for this patent
CC did not form part of the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 319 AA;
SQ
Query Match 87.9%; Score 29; DB 4; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 25
 AB027909
 ID AB027909 standard; protein: 319 AA.
 AC
 XX AB027909;
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #13436.
 XX
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS Enterobacter cloacae.
 PN W0200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002W0-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;
 XX
 DR WPI: 2003-029926/02.
 DR N-PSDB; ACA31779.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 PS
 XX Claim 25; SEQ ID NO 55833; 1766bp; English.
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pcr_sequences
 XX
 SQ Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PRRPYL 8
 DB 70 PRRPYL 76
 RESULT 26
 AB048247
 ID AB048247 standard; protein: 319 AA.
 XX
 AC AB048247;
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #33774.
 XX
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 OS *Salmonella typhi*.
 XX
 PN W0200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002W0-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;
 XX
 DR WPI: 2003-029926/02.
 DR N-PSDB; ACA52117.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 PS
 XX Claim 25; SEQ ID NO 76171; 1766bp; English.
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required

CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 319 AA;
Query Match 87.9%; Score 29; DB 6; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PRRPYXL 8
Db 70 PRRPYTL 76
RESULT 27
ABU37156
ID ABU37156 standard; protein; 319 AA.
XX
AC ABU37156;
XX
DT 23-OCT-2003 (revised)
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #22683.
XX
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Neisseria gonorrhoeae.
XX
PN MO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACAA1026.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 65080; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of
CC the 623 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences. (Updated on 23-OCT-2003 to
CC standardise OS field)
XX
SQ Sequence 319 AA;
Query Match 87.9%; Score 29; DB 6; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 PRRPYXL 8
Db 67 PRRPYTL 73
RESULT 28
ABU49488
ID ABU49488 standard; protein; 319 AA.
XX
AC ABU49488;
XX
DT 19-JUN-2003 (first entry)
XX
DE Protein encoded by Prokaryotic essential gene #35015.
XX
KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX
OS Vibrio cholerae.
XX
PN MO200277183-A2.
XX
PD 03-OCT-2002.
XX
PF 21-MAR-2002; 2002WO-US009107.
XX
PR 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.
XX
PA (ELIT-) ELITRA PHARM INC.
XX
PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX
DR WPI; 2003-029926/02.
DR N-PSDB; ACAA53358.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
PS Claim 25; SEQ ID NO 77412; 1766pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 319 AA;

Qy Query Match 87.9%; Score 29; DB 6; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2 PRRPYTL 8
 70 PRRPYTL 76

RESULT 29

ABU31682

ID ABU31682 standard; protein; 319 AA.

XX AC ABU31682;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #17209.

XX KM Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS *Klebsiella pneumoniae*.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

XX PR 06-SEP-2001; 2001US-00948993.

XX PR 25-OCT-2001; 2001US-0342923P.

XX PR 08-FEB-2002; 2002US-00072851.

XX PR 06-MAR-2002; 2002US-0362699P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

DR WPI; 2003-029926/02.

DR N-PSDB; ACA35552.

XX New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.

XX Claim 25; SEQ ID NO 59606; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 319 AA;

Qy Query Match 87.9%; Score 29; DB 6; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 2 PRRPYTL 8
 70 PRRPYTL 76

RESULT 30

ABU40645

ID ABU40645 standard; protein; 319 AA.

XX AC ABU40645;

XX DT 19-JUN-2003 (first entry)

XX DE Protein encoded by Prokaryotic essential gene #26172.

XX KM Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX OS *Proteus* sp.

XX PN WO200277183-A2.

XX PD 03-OCT-2002.

XX PF 21-MAR-2002; 2002WO-US009107.

XX PR 21-MAR-2001; 2001US-00815242.

ABU37970
 ID ABU37970 standard; protein; 319 AA.
 XX
 AC ABU37970;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #23497.
 XX
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR N-PSDB; ACA41840.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 65894; 1766bp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SO Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXPPLYL 8
 DB 67 PXPPLYL 73
 RESULT 33
 ID ABU47369
 AC ABU47369 standard; protein; 319 AA.
 XX
 AC ABU47369;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #32896.
 XX
 KM Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 OS *Salmonella typhimurium*.
 XX
 PN WO200277183-A2.
 XX
 PD 03-OCT-2002.
 XX
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX
 DR N-PSDB; ACA51239.
 XX
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 XX
 PS Claim 25; SEQ ID NO 75393; 1766bp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
 CC proliferation or the activity of a gene in an operon required for
 CC proliferation; (7) identifying a compound that influences the activity of
 CC the gene product or that has an activity against a biological pathway
 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
 CC product is overexpressed or underexpressed; (12) determining the extent
 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational

CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
Db 70 PRRPYTL 76

RESULT 34
ABU15268
ID ABU15268 standard; protein: 319 AA.
AC ABU15268;
XX
XX 19-JUN-2003 (first entry)
DT
XX
XX Protein encoded by Prokaryotic essential gene #795.
DE
XX
XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
KM
XX Escherichia coli.
OS
XX W0200277183-A2.
PN
XX
XX 03-OCT-2002.
PD
XX
XX 21-MAR-2002; 2002WO-US009107.
PF
XX
XX 21-MAR-2001; 2001US-00815242.
PR
XX 06-SEP-2001; 2001US-00948993.
PR
XX 25-OCT-2001; 2001US-0342923P.
PR
XX 08-FEB-2002; 2002US-00072851.
PR
XX 06-MAR-2002; 2002US-0362699P.
XX
XX
XX (ELIT-) ELITRA PHARM INC.
XX
XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;
XX WPI; 2003-0239926/02.
DR N-PSDB; ACA19138.
XX
XX New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.
XX
XX Claim 25; SEQ ID NO 43192; 1766bp; English.
XX
XX The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 319 AA;

Query Match 87.9%; Score 29; DB 6; Length 319;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PRRPYXL 8
Db 70 PRRPYTL 76

RESULT 35
ADD15500
ID ADD15500 standard; protein: 319 AA.
AC ADD15500;
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX Escherichia coli AccA protein (SeqID 65).
DE
XX
XX microbial; antimicrobial; membrane biosynthesis; pathogenic;
KM immunological response; vaccination; surface disinfectant;
KM personal hygiene application; food preservative; enzyme; AccA;
KM acetyl-CoA carboxylase carboxyl transferase subunit alpha.
XX
XX
XX Escherichia coli.
OS
XX W02003025007-A2.
PN
XX
XX 27-MAR-2003.
PD
XX
XX 20-SEP-2002; 2002WO-CA001428.
PF
XX
XX 21-SEP-2001; 2001US-0323992P.
PR
XX 21-SEP-2001; 2001US-0324152P.
PR
XX 25-SEP-2001; 2001US-0324692P.
PR
XX 26-OCT-2001; 2001US-0339924P.
PR
XX 29-OCT-2001; 2001US-0350973P.
PR
XX 30-OCT-2001; 2001US-0340924P.
PR
XX 27-NOV-2001; 2001US-0333666P.
PR
XX 18-DEC-2001; 2001US-0341732P.
PR
XX 18-DEC-2001; 2001US-0341776P.
PR
XX 19-DEC-2001; 2001US-0341949P.
XX
XX (AFFIT-) AFFINITUM PHARM INC.
XX
XX Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B;
PI Domagala M, Houston S, Kanagarajah D, Nethery K, Ng I, Mansoury K;
PI McDonald M, Pinder B, Viola C, Wrezel O;
XX WPI; 2003-468119/44.
DR N-PSDB; ADD15499.
XX
XX Novel crystallized recombinant polypeptides from *Staphylococcus aureus*,
PT

PT Streptococcus pneumoniae and Escherichia coli and which are involved in
 PT membrane biosynthesis, useful as targets for pathogenic bacteria.
 XX
 PS Claim 86; SEQ ID NO 65; 325pp; English.
 XX
 CC This invention relates to the structural and functional characterisation
 CC of microbial polypeptides from Staphylococcus aureus (S. aureus),
 CC Streptococcus pneumoniae (S. pneumoniae) and Escherichia coli (E. coli)
 CC that provide novel antimicrobial targets. Specifically, it refers to
 CC polypeptides that are involved in membrane biosynthesis, which play a
 CC critical role in the life cycle and viability of their pathogenic species
 CC of origin, and hence provide valuable drug targets. Furthermore, the
 CC invention describes modified version of these proteins that facilitate
 CC characterisation by labelling with isotopic or heavy atoms, and also
 CC fusion proteins. These proteins provide structural and functional
 CC information to aid the discovery of therapeutic molecules to treat
 CC disorders associated with a particular pathogenic species. As such, they
 CC are useful for inducing an immunological response in an individual and as
 CC an antigen for vaccination purposes. The polypeptides are also useful for
 CC developing antimicrobial agents for use as surface disinfectants,
 CC personal hygiene applications and as food preservatives or in treating
 CC food products to eliminate potential pathogens. This polypeptide sequence
 CC is the AccA protein encoded by DNA predicted from the genomic sequence of
 CC E. coli acetyl-CoA carboxylase carboxyl transferase subunit alpha of the
 CC invention.
 CC
 XX
 SQ Sequence 319 AA;
 Query Match 87.9%; Score 29; DB 7; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.Be+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXPYPYL 8
 Db 70 PXPYPYL 76
 RESULT 36
 ADD15502
 ID ADD15502 standard; protein: 319 AA.
 XX
 AC ADD15502;
 XX
 DT 15-JAN-2004 (first entry) -
 XX
 DE Escherichia coli AccA protein (SeqID 67).
 XX
 KW microbial; antimicrobial; membrane biosynthesis; pathogenic;
 KW immunological response; vaccination; surface disinfectant;
 KW personal hygiene application; food preservative; enzyme; AccA;
 KW acetyl-CoA carboxylase carboxyl transferase subunit alpha.
 XX
 OS Escherichia coli.
 XX
 PN WO2003025007-A2.
 PD 27-MAR-2003.
 PF 20-SEP-2002; 2002WO-CA001428.
 XX
 XX 21-SEP-2001; 2001US-0333992P.
 PR 21-SEP-2001; 2001US-0324152P.
 PR 25-SEP-2001; 2001US-0324692P.
 PR 26-OCT-2001; 2001US-0339924P.
 PR 29-OCT-2001; 2001US-0350973P.
 PR 30-OCT-2001; 2001US-0340924P.
 PR 27-NOV-2001; 2001US-0333666P.
 PR 18-DEC-2001; 2001US-0341732P.
 PR 18-DEC-2001; 2001US-0341776P.
 PR 19-DEC-2001; 2001US-0341949P.
 XX
 PA (AFTI-) AFFINITY PHARM INC.
 XX

PI Edwards A, Dharamsi A, Vedadi M, Alam MZ, Awrey D, Beattie B,
 PI Domagala M, Houston S, Kanagarajah D, Netherly K, Ng I, Mansoury K,
 PI McDonald M, Pinder B, Viola C, Wrezel O,
 XX
 DR WPI; 2003-468119/44.
 XX
 DR N-PSDB; ADD15501.
 XX
 PT Novel crystallized recombinant polypeptides from Staphylococcus aureus,
 PT Streptococcus pneumoniae and Escherichia coli and which are involved in
 PT membrane biosynthesis, useful as targets for pathogenic bacteria.
 XX
 PS Claim 86; SEQ ID NO 67; 325pp; English.
 XX
 CC This invention relates to the structural and functional characterisation
 CC of microbial polypeptides from Staphylococcus aureus (S. aureus),
 CC Streptococcus pneumoniae (S. pneumoniae) and Escherichia coli (E. coli)
 CC that provide novel antimicrobial targets. Specifically, it refers to
 CC polypeptides that are involved in membrane biosynthesis, which play a
 CC critical role in the life cycle and viability of their pathogenic species
 CC of origin, and hence provide valuable drug targets. Furthermore, the
 CC invention describes modified version of these proteins that facilitate
 CC characterisation by labelling with isotopic or heavy atoms, and also
 CC fusion proteins. These proteins provide structural and functional
 CC information to aid the discovery of therapeutic molecules to treat
 CC disorders associated with a particular pathogenic species. As such, they
 CC are useful for inducing an immunological response in an individual and as
 CC an antigen for vaccination purposes. The polypeptides are also useful for
 CC developing antimicrobial agents for use as surface disinfectants,
 CC personal hygiene applications and as food preservatives or in treating
 CC food products to eliminate potential pathogens. This polypeptide sequence
 CC is the AccA protein encoded by experimentally predicted DNA from E. coli
 CC acetyl-CoA carboxylase carboxyl transferase subunit alpha of the
 CC invention.
 CC
 XX
 SQ Sequence 319 AA;
 Query Match 87.9%; Score 29; DB 7; Length 319;
 Best Local Similarity 71.4%; Pred. No. 6.Be+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PXPYPYL 8
 Db 70 PXPYPYL 76
 RESULT 37
 ABU40545
 ID ABU40545 standard; protein: 320 AA.
 XX
 AC ABU40545;
 XX
 DT 19-JUN-2003 (first entry)
 XX
 DE Protein encoded by Prokaryotic essential gene #26072.
 XX
 KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
 KW Proteus sp.
 XX
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PF 21-MAR-2002; 2002WO-US009107.
 XX
 XX 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-00948993.
 PR 25-OCT-2001; 2001US-0342923P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;
XX WPI: 2003-029926/02.
DR N-PSDB; ACA44415.
XX
PT New antisense nucleic acids, useful for identifying proteins or screening
PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 68469; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
XX *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SO Sequence 320 AA;

Query Match 87.9%; Score 29; DB 6; Length 320;

Best Local Similarity 71.4%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXRPLYL 8
DB 71 PXRPLYL 77

RESULT 38

ABU23166
ID ABU23166 standard; protein; 321 AA.

AC ABU23166;

DT 19-JUN-2003 (first entry)

DE Protein encoded by prokaryotic essential gene #8693.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

OS Bordetella pertussis.

XX WO200277183-A2.

XX 03-OCT-2002.

XX

PF 21-MAR-2002; 2002WC-US009107.
XX
XX 21-MAR-2001; 2001US-00815242.
PR 06-SEP-2001; 2001US-00948993.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-00072851.
PR 06-MAR-2002; 2002US-0362699P.

XX (ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;

XX WPI: 2003-029926/02.

DR N-PSDB; ACA27036.

XX New antisense nucleic acids, useful for identifying proteins or screening
XX for homologous nucleic acids required for cellular proliferation to
XX isolate candidate molecules for rational drug discovery programs.

PS Claim 25; SEQ ID NO 51090; 1766bp; English.

XX The invention relates to an isolated nucleic acid comprising any one of
XX the 6213 antisense sequences given in the specification where expression
XX of the nucleic acid inhibits proliferation of a cell. Also included are:
XX (1) a vector comprising a promoter operably linked to the nucleic acid
XX encoding a polypeptide whose expression is inhibited by the antisense
XX nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX polypeptide or its fragment whose expression is inhibited by the
XX antisense nucleic acid; (4) an antibody capable of specifically binding
XX the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX proliferation or the activity of a gene in an operon required for
XX proliferation; (7) identifying a compound that influences the activity of
XX the gene product or that has an activity against a biological pathway
XX required for proliferation, or that inhibits cellular proliferation; (8)
XX identifying a gene required for cellular proliferation or the biological
XX pathway in which a proliferation-required gene or its gene product lies
XX or a gene on which the test compound that inhibits proliferation of an
XX organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX compound's activity; (11) a culture comprising strains in which the gene
XX product is overexpressed or underexpressed; (12) determining the extent
XX to which each of the strains is present in a culture or collection of
XX strains; or (13) identifying the target of a compound that inhibits the
XX proliferation of an organism. The antisense nucleic acids are useful for
XX identifying proteins or screening for homologous nucleic acids required
XX for cellular proliferation to isolate candidate molecules for rational
XX drug discovery programs, or for screening homologous nucleic acids
XX required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
XX *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
XX the target prokaryotic essential genes. Note: The sequence data for this
XX patent did not form part of the printed specification, but was obtained
XX in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SO Sequence 321 AA;

Query Match 87.9%; Score 29; DB 6; Length 321;

Best Local Similarity 71.4%; Pred. No. 6.9e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 PXRPLYL 8
DB 67 PXRPLYL 73

RESULT 39

ABU22657
ID ABU22657 standard; protein; 323 AA.

AC ABU22657;

DT 19-JUN-2003 (first entry)

XX

DE Protein encoded by Prokaryotic essential gene #8184.
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX Burkholderia mallei.
 OS
 XX WO200277183-A2.
 XX
 XX 03-OCT-2002.
 XX
 XX 21-MAR-2002; 2002WO-US009107.
 XX
 XX 21-MAR-2001; 2001US-00815242.
 XX 06-SEP-2001; 2001US-00948993.
 XX 25-OCT-2001; 2001US-0342923P.
 XX 08-FEB-2002; 2002US-00072851.
 XX 06-MAR-2002; 2002US-0362699P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 XX
 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 XX N-PSDB; ACAA2527.
 DR
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 PS
 PS Claim 25; SEQ ID NO 50581; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
 CC (1) a vector comprising a promoter operably linked to the nucleic acid
 CC encoding a polypeptide whose expression is inhibited by the antisense
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
 CC polypeptide or its fragment whose expression is inhibited by the
 CC antisense nucleic acid; (4) an antibody capable of specifically binding
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 CC required for proliferation, or that inhibits cellular proliferation; (8)
 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
 CC compound's activity; (11) a culture comprising strains in which the gene
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 CC to which each of the strains is present in a culture or collection of
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 CC patent did not form part of the printed specification, but was obtained
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 CC ftp.wipo.int/pub/published_pct_sequences
 XX

SO Sequence 323 AA;

Query Match 87.9%; Score 29; DB 6; Length 323;
 Best Local Similarity 71.4%; Pred. No. 6.9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PXXRYXL 8
 DB 67 PQRBYTL 73

RESULT 40
 ABU19773
 ID ABU19773 standard; protein; 323 AA.
 XX
 XX AC ABU19773;
 XX
 XX DT 19-JUN-2003 (first entry)
 XX
 XX DE Protein encoded by Prokaryotic essential gene #5300.
 XX
 XX Antisense; prokaryotic essential gene; cell proliferation; drug design.
 XX
 XX Borrelia cepacia.
 OS
 XX WO200277183-A2.
 XX
 XX 03-OCT-2002.
 XX
 XX 21-MAR-2002; 2002WO-US009107.
 XX
 XX 21-MAR-2001; 2001US-00815242.
 XX 06-SEP-2001; 2001US-00948993.
 XX 25-OCT-2001; 2001US-0342923P.
 XX 08-FEB-2002; 2002US-00072851.
 XX 06-MAR-2002; 2002US-0362699P.
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 XX (ELIT-) ELITRA PHARM INC.
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 XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW,
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
 XX WPI; 2003-029926/02.
 XX N-PSDB; ACAA2527.
 DR
 PT New antisense nucleic acids, useful for identifying proteins or screening
 PT for homologous nucleic acids required for cellular proliferation to
 PT isolate candidate molecules for rational drug discovery programs.
 PS
 PS Claim 25; SEQ ID NO 47697; 1766pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising any one of
 CC the 6213 antisense sequences given in the specification where expression
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:
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 CC identifying a gene required for cellular proliferation or the biological
 CC pathway in which a proliferation-required gene or its gene product lies
 CC or a gene on which the test compound that inhibits proliferation of an
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
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 CC to which each of the strains is present in a culture or collection of
 CC strains; or (13) identifying the target of a compound that inhibits the
 CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
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 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
 CC the target prokaryotic essential genes. Note: The sequence data for this
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 Best Local Similarity 71.4%; Pred. No. 6.9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PRRPYXL 8
 | | | | |
 Db 67 PRRPYTL 73

Search completed: March 28, 2005, 08:35:06
 Job time : 72 secs

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